

GenCore version 5.1.5
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2003, 05:43:36 ; Search time 829 Seconds

(without alignments)
111.178 Million cell updates/sec

Title:

Perfect score: 399

Sequence: 1 MSGSLPVLVLLTLGSSHGT.....SGTSTVLHARSQHVVVNCVT 78

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 746064 seqs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q-/cgn2_1/USPTO_spool/US09092296/runat_30042003_133104_14466/app_query.fasta_1.263
-DB-PublishedApplications_NA -OFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-MAXLEN=2000000000 -USER=US09092296.ecgn_1_1.88_@runat_30042003_133104_14466
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-DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10
-XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications.NA.*
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	399	100.0	413	9	US-09-092-296-6
2	399	100.0	422	9	US-09-992-598-362
3	399	100.0	422	9	US-09-989-293A-362
4	399	100.0	422	9	US-10-063-547-65

5	399	100.0	422	9	US-09-989-735-362
6	399	100.0	422	9	US-09-990-444-362
7	399	100.0	422	9	US-09-989-730-362
8	399	100.0	422	9	US-09-990-436-362
9	399	100.0	422	9	US-09-991-181-362
10	399	100.0	422	9	US-09-993-687-362
11	399	100.0	422	9	US-09-989-734-362
12	399	100.0	422	9	US-09-997-653-362
13	399	100.0	422	9	US-10-174-590-241
14	399	100.0	422	9	US-10-176-758-241
15	399	100.0	422	9	US-10-063-616-65
16	399	100.0	422	9	US-10-173-737-241
17	399	100.0	422	9	US-09-993-667-362
18	399	100.0	422	9	US-10-063-502-65
19	399	100.0	422	9	US-10-173-706-241
20	399	100.0	422	9	US-10-175-738-241
21	399	100.0	422	9	US-10-175-752-241
22	399	100.0	422	9	US-10-176-482-241
23	399	100.0	422	9	US-10-176-757-241
24	399	100.0	422	9	US-10-176-913-241
25	399	100.0	422	9	US-10-180-552-241
26	399	100.0	422	9	US-10-180-557-241
27	399	100.0	422	9	US-09-990-438-362
28	399	100.0	422	9	US-09-990-562-362
29	399	100.0	422	9	US-09-997-428-362
30	399	100.0	422	9	US-09-997-666-362
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37	399	100.0	422	9	US-10-175-740-241
38	399	100.0	422	9	US-10-175-743-241
39	399	100.0	422	9	US-10-176-488-241
40	399	100.0	422	9	US-10-176-492-241
41	399	100.0	422	9	US-10-176-747-241
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43	399	100.0	422	9	US-10-176-985-241
44	399	100.0	422	9	US-10-176-987-241
45	399	100.0	422	9	US-10-176-991-241

ALIGNMENTS

RESULT 1
US-09-092-296-6
; Sequence 6, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-092-296-6

Alignment Scores:
Pred. No.: 4,02e-49 Length: 413
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-092-296-15 (1-78) x US-09-092-296-6 (1-413)

Qy 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 47 ATGGGGTCTGGGTCGCCCTTGTCTCTTGACCCCTCTGGCAGCTCACATGAACA 106
Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 107 GGGCGGGGTATGACTTTGCAACTGAAGTGAAGGAGTCTTTCTGCAAAATTCCTCCTAT 166
Qy 41 GluSerSerPheLeuLeuLeuLeuLysLeuLysLeuLeuHisLeuLeuProSerGly 60
Db 167 GAGTCACGCTTCCTGGAAATGCTTGAAAGCTCTGCCCTCTCCCTCCATCTCCCTCAGGG 226
Qy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 227 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTGTCTGCAACACA 280

RESULT 2
US-09-992-598-362
; Sequence 362, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US/09/992,598
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
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; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-01
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; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-092-296-15 (1-78) x US-09-989-293A-362 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuThrLeuLeuGlySerHisGlyThr 20
Db 58 ATGGGGTCTGGGCTGCCCTTGCTCTTGACCCCTCTTGGCAGCTCACATGGAACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerTyr 40
Db 118 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuLysLeuCysLeuLeuHisLeuProSerGly 60
Db 178 GAGTCCAGCTTCTGGAATTCCTGAAAGCTCTGCCTCTCTCCATCTCCCTTCAGGG 237
QY 61 ThrSerValThrLeuHisAlaArgSerGlnHisValValCysAsnThr 78
Db 238 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 4

US-10-063-547-65
; Sequence 65, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan I.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-547-65

Alignment Scores:

Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-092-296-15 (1-78) x US-10-063-547-65 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuThrLeuLeuGlySerHisGlyThr 20
Db 58 ATGGGGTCTGGGCTGCCCTTGCTCTTGACCCCTCTTGGCAGCTCACATGGAACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerTyr 40
Db 118 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuLysLeuCysLeuLeuHisLeuProSerGly 60
Db 178 GAGTCCAGCTTCTGGAATTCCTGAAAGCTCTGCCTCTCTCCATCTCCCTTCAGGG 237
QY 61 ThrSerValThrLeuHisAlaArgSerGlnHisValValCysAsnThr 78
Db 238 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 5

US-09-989-735-362
; Sequence 362, Application US/09989735
; Publication No. US20020193299A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.	PRIOR APPLICATION NUMBER: 60/088822	PRIOR FILING DATE: 1998-06-10
APPLICANT: Williams, P. Mickey	PRIOR APPLICATION NUMBER: 60/088858	PRIOR FILING DATE: 1998-06-11
APPLICANT: Wood, William I.	PRIOR APPLICATION NUMBER: 60/088861	PRIOR FILING DATE: 1998-06-11
APPLICANT: Zhang, Zemin	PRIOR APPLICATION NUMBER: 60/088876	PRIOR FILING DATE: 1998-06-11
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	PRIOR APPLICATION NUMBER: 60/089105	PRIOR FILING DATE: 1998-06-12
FILE OF INVENTION: Acids Encoding the Same	PRIOR APPLICATION NUMBER: 60/089440	PRIOR FILING DATE: 1998-06-16
FILE REFERENCE: P273021C61	PRIOR APPLICATION NUMBER: 60/089512	PRIOR FILING DATE: 1998-06-16
CURRENT APPLICATION NUMBER: US/09/989,735	PRIOR APPLICATION NUMBER: 60/089514	PRIOR FILING DATE: 1998-06-16
CURRENT FILING DATE: 2001-11-19	PRIOR APPLICATION NUMBER: 60/089532	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/049787	PRIOR APPLICATION NUMBER: 60/089538	PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1997-06-16	PRIOR APPLICATION NUMBER: 60/089598	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/062250	PRIOR APPLICATION NUMBER: 60/089599	PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1997-10-17	PRIOR APPLICATION NUMBER: 60/089600	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/065186	PRIOR APPLICATION NUMBER: 60/089653	PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1997-11-13	PRIOR APPLICATION NUMBER: 60/089908	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/066770	PRIOR APPLICATION NUMBER: 60/089947	PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1997-11-24	PRIOR APPLICATION NUMBER: 60/089948	PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-02-25	PRIOR APPLICATION NUMBER: 60/090246	PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/078910	PRIOR APPLICATION NUMBER: 60/090252	PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/090254	PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/084600	PRIOR APPLICATION NUMBER: 60/090429	PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/090431	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/087106	PRIOR APPLICATION NUMBER: 60/090435	PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-05-28	PRIOR APPLICATION NUMBER: 60/090444	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/087607	PRIOR APPLICATION NUMBER: 60/090445	PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/090472	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/087609	PRIOR APPLICATION NUMBER: 60/090535	PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/090540	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/087759	PRIOR APPLICATION NUMBER: 60/090542	PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/090557	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/087827	PRIOR APPLICATION NUMBER: 60/090676	PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-03	PRIOR APPLICATION NUMBER: 60/090678	PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/088021		
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PRIOR FILING DATE: 1998-06-10		

; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-092-296-15 (1-78) x US-09-989-735-362 (1-422)

Qy 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 58 ATGGGTCFVGCGCTGCCCCCTTGCTCTCTTGACCTCTCTGGCAGCTCATATGGAACA 117
Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 118 GGCCCGGTATGACTTTGCCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177
Qy 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
Db 178 GAGTCAGCTTCCTGGAAATTCCTGAAAGCTCTGCTCTCTCTCTCTCTCTCTCTCAGG 237
Qy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 238 ACCAGCGTCACCCCTCACCATCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 6

US-09-990-444-362
; Sequence 362, Application US/0990444
; Publication No. US2002019300A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
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; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-06-05
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; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09

[illegible]

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C69
; CURRENT APPLICATION NUMBER: US/09/989,730
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Dbs: 9 Gaps: 0

US-09-092-296-15 (1-78) x US-09-989-730-362 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuGlySerHisGlyThr 20
Db 58 ATGGGGCTGGGCTGGCCCTTGTCTCTTGGACCTCTTGGCAGCTCATGGAACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuGlySerPheLeuThrAsnSerSerTyr 40
Db 118 GGCCCGGTATGACTTTGCAACTTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuLeuHisLeuProSerGly 60
Db 178 GAGTCCAGCTTCTGGAATGCTTGAAAGCTCTGCCTCTCTCTCTCTCTCTCTCTCAGG 237

QY 61 ThrSerValThrIleuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 238 ACCAGCGTCACCTCCACCATGCAGATCTCAACACCATGTTGCTGCAACACA 291
RESULT 8
US-09-990-436-362
; Sequence 362, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C14
; CURRENT APPLICATION NUMBER: US/09/990,436
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
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; PRIOR APPLICATION NUMBER: 60/088028
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; PRIOR APPLICATION NUMBER: 60/088326
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; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252

; PRIOR FILING DATE: 1998-06-22
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; PRIOR FILING DATE: 1998-06-22
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; PRIOR FILING DATE: 1998-06-23
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; PRIOR APPLICATION NUMBER: 60/090444
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
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; PRIOR APPLICATION NUMBER: 60/090694
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	4.15e-49	Length:	422
Score:	399.00	Matches:	78
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DE:	9	Gaps:	0

US-09-092-296-15 (1-78) x US-09-990-436-362 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuThrLeuLeuGlySerHisGlyThr 20

; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
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; PRIOR APPLICATION NUMBER: 60/090246
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; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-092-296-15 (1-78) x US-09-991-181-362 (1-422)

Qy 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 58 ATGGGCTCGGGCTGGCCCTTGCTCTTGACCTCTCTGGCAGCTCATGGAACA 117
Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 118 GGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGCACAAATCTCCTAT 177
Qy 41 GluSerSerPheLeuGluLeuLeuGluLysLeuLysCysLeuLeuHisLeuProSerGly 60
Db 178 GATCCAGCTTCCTGGAAATGCTTGAAGAAGCTCTGCCCTCTCCATCTCCCTCAGG 237
Qy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 238 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 10
US-09-993-687-362
; Sequence 362, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C11
; CURRENT APPLICATION NUMBER: US/09/993,687
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 4.15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-092-296-15 (1-78) x US-09-993-687-362 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuGlySerSerHisGlyThr 20
DB 58 ATGGGTCTGGGCTGCCCTTGTCTCTCTTGACCTCTCTGGCAGCTCACATGGAACA 117

QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
DB 118 GGCCCGGATGACTTTCACACTGAGCTGAGGAGTCTTTCTGACAAATTCCTCTAT 177

QY 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
DB 178 GAGTCCAGCTCTCGGAATTCCTGTAAGGCTTCGCCCTCTCTCCATCTCCCTTCAGGG 237

QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
DB 238 ACCAGGTCACCTCCACCATGCAGATCTCAACACCATGTGTGTGCAACACA 291

RESULT 11
US-09-989-734-362
; Sequence 362, Application US/09989734
; Publication No. US2003000351A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavio, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C64
; CURRENT APPLICATION NUMBER: US/09/989,734
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/088025
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; PRIOR APPLICATION NUMBER: 60/088026
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; PRIOR APPLICATION NUMBER: 60/088167
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512

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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC38
; CURRENT APPLICATION NUMBER: US/09/997,653
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
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; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25

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; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-241
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Alignment Scores:
Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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US-09-092-296-15 (1-78) x US-10-174-590-241 (1-422)

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QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuGlySerSerHisGlyThr 20
    |||||||
Db 58 ATGGGGTCTGGGCTGCCCTTGTCTTGTGACCTCTTGGCAGCTCAGTGAACA 117
    |||||||
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuGluSerPheLeuThrAsnSerSerTyr 40
    |||||||
Db 118 GGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177
    |||||||
QY 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
    |||||||
Db 178 GAGTCAGCTTCTCGGAATTGCTTGAAGAGCTCTGCCTCTCTCCATCTCCCTTCAGG 237
    |||||||
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
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Db 238 ACCAGGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291
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RESULT 14

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US-10-176-758-241
; Sequence 241, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-758-241
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Alignment Scores:
Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
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; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
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; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR FILING DATE: 1998-07-09
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Alignment Scores:
Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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US-09-092-296-15 (1-78) x US-09-997-653-362 (1-422)

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Db 58 ATGGGGTCTGGGCTGCCCTTGTCTTGTGACCTCTTGGCAGCTCAGTGAACA 117
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QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuGluSerPheLeuThrAsnSerSerTyr 40
    |||||||
Db 118 GGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177
    |||||||
QY 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
    |||||||
Db 178 GAGTCAGCTTCTCGGAATTGCTTGAAGAGCTCTGCCTCTCTCCATCTCCCTTCAGG 237
    |||||||
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
    |||||||
Db 238 ACCAGGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291
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RESULT 13

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US-10-174-590-241
; Sequence 241, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-21
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-241
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Job time : 831 secs

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US-09-092-296-15 (1-78) x US-10-176-758-241 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerHisGlyThr 20
Db 58 ATGGGGTCTGGGCTGCCCTTGTCTCTTGCACCTCCTTGCAGCTCACATGAACA 117

QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 118 GGCGCGGTATGACTTGAACCTGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCCTAT 177

QY 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
Db 178 GAGTCCAGCTTCCTGGAATTGCTGAAAAGCTCTGCCTCCTCCTCATCTCCCTTCAGGG 237

QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 238 ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 15
US-10-063-616-65
; Sequence 65, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-65

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Pred. No.: 4.15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-092-296-15 (1-78) x US-10-063-616-65 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerHisGlyThr 20
Db 58 ATGGGGTCTGGGCTGCCCTTGTCTCTTGCACCTCCTTGCAGCTCACATGAACA 117

QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 118 GGCGCGGTATGACTTGAACCTGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCCTAT 177

QY 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
Db 178 GAGTCCAGCTTCCTGGAATTGCTGAAAAGCTCTGCCTCCTCCTCATCTCCCTTCAGGG 237

QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 238 ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291
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GenCore version 5.1.5
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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)

385.819 Million cell updates/sec

Title: US-09-092-296-15

Perfect score: 399

Sequence: 1 MGSGLPLVLLTLTGSSHGT.....SGTSVTLHARSQHVVVNCVT 78

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-USER=US09092296.@cgn_1_36@runat_30042003_133103_14436 -NCFU=6 -ICPU=3
-NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 4	68	17.0	3195	2	US-08-951-648-5
c 5	68	17.0	3195	3	US-09-174-437-5
c 6	68	17.0	111282	4	US-09-754-250-3
c 7	67.5	16.9	2835	4	US-09-134-001C-1515
c 8	67.5	16.9	3561	4	US-09-134-001C-1685
c 9	67.5	16.9	6414	4	US-09-134-001C-1626
c 10	67	16.8	5892	3	US-08-753-587-27
c 11	67	16.8	7240	3	US-08-755-587-15
c 12	67	16.8	11283	2	US-08-603-753D-3

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c 17	67	16.8	11385	3	US-09-044-908-1
c 18	66.5	16.7	1867	1	US-07-772-087-1
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c 21	65	16.3	4389	2	US-08-951-648-3
c 22	65	16.3	4389	3	US-09-174-437-3
c 23	64.5	16.2	2680	1	US-08-588-821-1
c 24	64.5	16.2	2680	1	US-08-913-214-1
c 25	64.5	16.2	2680	2	US-09-005-532-1
c 26	64.5	16.2	2680	3	US-09-255-888-1
c 27	64.5	16.2	2680	4	US-09-312-748-3
c 28	64	16.0	1687	4	US-08-630-915A-191
c 29	64	16.0	4002	2	US-08-231-193A-49
c 30	64	16.0	4002	2	US-08-486-273A-53
c 31	64	16.0	4002	3	US-08-480-474-53
c 32	64	16.0	4002	3	US-08-940-086A-53
c 33	64	16.0	4002	4	US-08-940-035A-53
c 34	64	16.0	4002	4	US-08-935-105A-53
c 35	64	16.0	4002	4	US-09-648-797-53
c 36	64	16.0	4017	2	US-08-231-193A-49
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c 38	64	16.0	4017	3	US-08-480-474-49
c 39	64	16.0	4017	3	US-08-940-086A-49
c 40	64	16.0	4017	4	US-08-940-035A-49
c 41	64	16.0	4017	4	US-08-935-105A-49
c 42	64	16.0	4017	4	US-09-648-797-49
c 43	64	16.0	4053	2	US-08-231-193A-47
c 44	64	16.0	4053	2	US-08-486-273A-47
c 45	64	16.0	4053	3	US-08-480-474-47

ALIGNMENTS

RESULT 1
US-08-405-254-9/c
; Sequence 9, Application US/08405254
; Patent No. 5773288
; GENERAL INFORMATION:
; APPLICANT: BRIGGS, STEVEN P.
; APPLICANT: BENSON, ROBERT J.
; TITLE OF INVENTION: PLANT GENES AFFECTING GIBBERELLIC ACID
; TITLE OF INVENTION: BIOSYNTHESIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K STREET, NW, SUITE 500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,254
; FILING DATE: 16-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,465
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, STEPHEN A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 33229/299/PIHI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399

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; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-405-254-9

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Score: 69.00 Matches: 26
Percent Similarity: 37.76% Conservative: 11
Best Local Similarity: 26.53% Mismatches: 29
Query Match: 17.29% Indels: 32
DB: 1 Gaps: 3

US-09-092-296-15 (1-78) x US-08-405-254-9 (1-2520)
Qy 7 LeuValLeuLeuThrLeuLeuGlySerSerHisGlyThrGlyProGlyMet----- 24
Db 2128 CTCCTCCCTGCTGCTGCTTTGCCACGGATACGGATCGGATCGGATCGGACCTG 2069
Qy 25 -----ThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAnSerSerTyrGluSer 42
Db 2068 ATTGACGAGCTGCAGCTGCAGCGCAAGTGAAGCAGAAAGCAAGACGCGGTGAGGAAC 2009
Qy 43 SerPheLeuGluLeuLeuLulys----- 50
Db 2008 TCGACCATCAGGACACACAAAGAGCTAGCCTAGCAGCAGCGCCTGACTG 1949
Qy 51 -----LeuCysLeuLeuLeuHisLeuPro 58
Db 1948 CTGCCTGCCTCTCCATCTGCTATGTTTCTTTGTCTGATGCCATCTGCGCT 1889
Qy 59 SerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCys 76
Db 1888 -----GTGTGTGTGGCTACCTAAGACGACGACGACTTGTCTGT 1847

RESULT 2
US-09-780-049-18
; Sequence 18, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09780,049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 18
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-780-049-18

Alignment Scores:
Pred. No.: 772 Length: 40000
Score: 69.00 Matches: 22
Percent Similarity: 40.00% Conservative: 12
Best Local Similarity: 25.88% Mismatches: 15
Query Match: 17.29% Indels: 36
DB: 4 Gaps: 3

US-09-092-296-15 (1-78) x US-09-780-049-18 (1-40000)
Qy 5 LeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThrGlyPro----- 22
Db 20067 ATTCCAGTCTCCAAATTTCTGACTTTATTAGGGGAAGGAATGGCGATTGTTTGT 20126
```

```
QY 23 -----GlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeu 35
Db 20127 TTTGTTTGGACAGAGTCTTTGCTCTCACCCAGCTGGAGTGCAGTATCGATCTTG 20186
QY 36 ThrAnSerSerTyrGluSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuLeu 55
Db 20187 GCTCAGCGCAAC-----CTC 20201
QY 56 HisLeuProSer-----GlyThrSerVal 63
Db 20202 CACCTCCCAAGTTTAAGCAATTCCTCTGCCTCAGCTCCCAAGTAGCTGTACTACAGTC 20261
QY 64 ThrLeuHisHisAla 68
Db 20262 ATGACCAACCATGCC 20276

RESULT 3
US-09-238-303-7
; Sequence 7, Application US/09238303B
; Patent No. 6284253
; GENERAL INFORMATION:
; APPLICANT: Barr, Margaret C.
; TITLE OF INVENTION: No. 6284253el Feline Immunodeficiency Virus Nucleotide Sequence
; FILE REFERENCE: 18617.0059
; CURRENT APPLICATION NUMBER: US/09/238,303B
; CURRENT FILING DATE: 1999-01-28
; EARLIER APPLICATION NUMBER: US 60/072,927
; EARLIER FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 7
; LENGTH: 9751
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: recombinant viral clone constructed from the genomic DNA of
; OTHER INFORMATION: a Pallas's cat feline immunodeficiency virus
US-09-238-303-7

Alignment Scores:
Pred. No.: 125 Length: 9751
Score: 68.50 Matches: 24
Percent Similarity: 47.30% Conservative: 11
Best Local Similarity: 32.43% Mismatches: 34
Query Match: 17.17% Indels: 5
DB: 4 Gaps: 2

US-09-092-296-15 (1-78) x US-09-238-303-7 (1-9751)
QY 2 GlySerGlyLeuProLeuValLeuLeuThr-----LeuLeuGlySerSer 17
Db 8384 GGATTAGGATTAACCTAGCTCTTGTACTGTCTACACTGCAGGGTTAATAGGAACAACA 8443
QY 18 HisGlyThrGlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAn 37
Db 8444 ACGGGGACATCT---GCACGTGCAGTGTCTATTAAATTAAGAAGTGTATTAACAACA 8500
QY 38 SerSerTyrGluSerSerPheLeuGluLeuGluLysLeuCysLeuLeuLeuHisLeu 57
Db 8501 TCACAAATAAATGAACACATCTGGGATGTTAAATCTTACAAAGACACTAAACAG 8560
QY 58 ProSerGlyThrSerValThrLeuHisHisAlaArgSerGln 71
Db 8561 GCAGAAAGAGTGTATTTTAAACGTTACATCAGAGAGTATCTAGG 8602

RESULT 4
US-08-951-648-5/c
; Sequence 5, Application US/08951648
; Patent No. 5932465
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker, Sears Tower Suite 6300
CITY: Chicago
STATE: Illinois
COUNTRY: US
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,648
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/34038
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 67..2403
US-08-951-648-5

Alignment Scores:
Pred. No.: 30.4 Length: 3195
Score: 68.00 Matches: 26
Percent Similarity: 42.53% Conservative: 11
Best Local Similarity: 29.89% Mismatches: 29
Query Match: 17.04% Indels: 21
DB: 2 Gaps: 3

US-09-092-296-15 (1-78) x US-08-951-648-5 (1-3195)

QY 3 SerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThrGlyPro 22
Db 1090 TCAGGACTCCCGTCTCTGCTACTT-----GGCCAG 1058
QY 23 GlyMetThrLeuGlnLeuLeuLeuGlySerPhe-LeuThrAsnSerSerTyrGluSe 42
Db 1057 CAATTCCTTCTCAATTGAAATCTTATCTCTTGTGCTCTTGAAGACAGGTTTTCCTT 998
QY 42 rSerPheLeuGluLeuLeuGlyLys-----LeuCysLeuLeuHisLe 57
Db 997 CTTTCTCTCCATATCAAAAAGGCTGAATATACTCTTCTTATGTCACCT 938
QY 57 uProSerGlyThrSerValThrLeuHisAlaArgSerGlnHisValVal----- 75
Db 937 GGAAGAGTCACACGATCGGCATTCACCAGGTTTTTGGCATATATCATTTGTTCAA 878
QY 76 -----CysAsn 77
Db 877 GTAGAGAACTATTGCAAC 859

RESULT 5

US-09-174-437-5/C
; Sequence 5, Application US/09174437A
; Patent No. 6133007
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/174,437A

; CURRENT FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 08/951,648
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 3195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(2403)
US-09-174-437-5

Alignment Scores:

Pred. No.: 30.4 Length: 3195
Score: 68.00 Matches: 26
Percent Similarity: 42.53% Conservative: 11
Best Local Similarity: 29.89% Mismatches: 29
Query Match: 17.04% Indels: 21
DB: 3 Gaps: 3

US-09-092-296-15 (1-78) x US-09-174-437-5 (1-3195)

QY 3 SerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThrGlyPro 22
Db 1090 TCAGGACTCCCGTCTCTGCTACTT-----GGCCAG 1058
QY 23 GlyMetThrLeuGlnLeuLeuLeuGlySerPhe-LeuThrAsnSerSerTyrGluSe 42
Db 1057 CAATTCCTTCTCAATTGAAATCTTATCTCTTGTGCTCTTGAAGACAGGTTTTCCTT 998
QY 42 rSerPheLeuGluLeuLeuGlyLys-----LeuCysLeuLeuHisLe 57
Db 997 CTTTCTCTCCATATCAAAAAGGCTGAATATACTCTTCTTATGTCACCT 938
QY 57 uProSerGlyThrSerValThrLeuHisAlaArgSerGlnHisValVal----- 75
Db 937 GGAAGAGTCACACGATCGGCATTCACCAGGTTTTTGGCATATATCATTTGTTCAA 878
QY 76 -----CysAsn 77
Db 877 GTAGAGAACTATTGCAAC 859

RESULT 6

US-09-754-250-3/C
; Sequence 3, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063
; CURRENT APPLICATION NUMBER: US/09/754,250
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 111282
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(111282)
; OTHER INFORMATION: n = A,T,C or G
US-09-754-250-3

Alignment Scores:

Pred. No.: 4.42e+03 Length: 111282
Score: 68.00 Matches: 19
Percent Similarity: 56.82% Conservative: 6
Best Local Similarity: 43.18% Mismatches: 19

Db 4924 ACATACCTCGTTGAATCTGAAGACTCGTACTTGGTACTTCACTTAATGACGTACTTGCAC 4865
 QY 37 AsnSerSerTyGluSerSer-----PheLeuGluLeu----- 47
 Db 4864 TATTCGAGTCATCAGTCTGTTGATGTTGACGACATTTCTGACGTGTGACGGCTTGTG 4805
 QY 48 ---LeuGluLeuLeuLeuHisLeuProSerGlyThrSerValThrLeuHis 66
 Db 4804 AATCTGAACGCTTGTGTTACTGATTCACCTTG-----ATGACGTACTTG 4760
 QY 67 HisAlaArgSerGlnHisValVal 75
 Db 4759 CACTGTCCGAGTCGCTCTCACTTGTG 4733

RESULT 10
 US-08-755-587-27/c
 ; Sequence 27, Application US/08755587
 ; Patent No. 6045997
 ; GENERAL INFORMATION:
 ; APPLICANT: Futreal, Phillip A
 ; APPLICANT: Wooster, Richard F
 ; APPLICANT: Ashworth, Alan
 ; APPLICANT: Stratton, Michael R
 ; TITLE OF INVENTION: Materials and methods relating to the
 ; TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer
 ; TITLE OF INVENTION: susceptibility gene and uses thereof.
 ; NUMBER OF SEQUENCES: 222
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bell Seltzer Park & Gibson
 ; STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
 ; CITY: Raleigh
 ; STATE: NC
 ; COUNTRY: USA
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/755,587
 ; FILING DATE: 25-NOV-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9523959.6
 ; FILING DATE: 23-NOV-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9525555.0
 ; FILING DATE: 14-DEC-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9617961.9
 ; FILING DATE: 28-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kenneth D Sibley
 ; REGISTRATION NUMBER: 31,665
 ; REFERENCE/DOCKET NUMBER: 5405-135
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5892 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 483..5412
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 481..5412
 US-08-755-587-27

Alignment Scores:
 Pred. No.: 97.8 Length: 5892
 Score: 67.00 Matches: 16

Percent Similarity: 51.11% Conservative: 7
 Best Local Similarity: 35.56% Mismatches: 22
 Query Match: 16.79% Indels: 0
 DB: 3 Gaps: 0
 US-09-092-296-15 (1-78) x US-08-755-587-27 (1-5892)
 QY 27 GlnLeuLeuLeuLeuGluSerPheLeuThrAsnSerSerTyGluSerSerPheLeuGlu 46
 Db 3430 AAATTATCATTTAGACCTTAGTGGCACCACAGTCTCAATAGAACAAAGGTTTTTATCA 3371
 QY 47 LeuLeuGluLeuLeuLeuHisLeuProSerGlyThrSerValThrLeuHis 66
 Db 3370 TTATTGAGAGATTTCTTACATTTTGTACATTTGGGCGACGTGTGATCTCAATGCTCA 3311
 QY 67 HisAlaArgSerGln 71
 Db 3310 CATGCTAATTCAGG 3296

RESULT 11
 US-08-755-587-15/c
 ; Sequence 15, Application US/08755587
 ; Patent No. 6045997
 ; GENERAL INFORMATION:
 ; APPLICANT: Futreal, Phillip A
 ; APPLICANT: Wooster, Richard F
 ; APPLICANT: Ashworth, Alan
 ; APPLICANT: Stratton, Michael R
 ; TITLE OF INVENTION: Materials and methods relating to the
 ; TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer
 ; TITLE OF INVENTION: susceptibility gene and uses thereof.
 ; NUMBER OF SEQUENCES: 222
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bell Seltzer Park & Gibson
 ; STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
 ; CITY: Raleigh
 ; STATE: NC
 ; COUNTRY: USA
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/755,587
 ; FILING DATE: 25-NOV-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9523959.6
 ; FILING DATE: 23-NOV-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9525555.0
 ; FILING DATE: 14-DEC-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9617961.9
 ; FILING DATE: 28-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kenneth D Sibley
 ; REGISTRATION NUMBER: 31,665
 ; REFERENCE/DOCKET NUMBER: 5405-135
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7240 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 US-08-755-587-15

Alignment Scores:
 Pred. No.: 131 Length: 7240
 Score: 67.00 Matches: 16
 Percent Similarity: 51.11% Conservative: 7
 Best Local Similarity: 35.56% Mismatches: 22

```
Query Match: 16.79% Indels: 0
DB: 3 Gaps: 0
US-09-092-296-15 (1-78) x US-08-755-587-15 (1-7240)

QY 27 GlnLeuLysLeuLysSerPheLeuThrAsnSerSerTyrGluSerSerPheLeuGlu 46
Db 4015 AAATTATCATCTTAAGAGCTTAGGTGGCACACAGTCTCAATAGAAACAAGGTTTTTATCA 3956
QY 47 LeuLeuGluLysLeuLysLeuLeuLeuHisLeuProSerGlyThrSerValThrLeuHis 66
Db 3955 TTATTGAGAGAATTCTGCATCTTTACACTTTGGGCAGCTGTGATCTCAATGGTCTCA 3896
QY 67 HisalaArgSerGln 71
Db 3895 CATGCTAATTC AAGG 3881

RESULT 12
US-08-603-753D-3/C
; Sequence 3, Application US/08603753D
; Patent No. 5891857
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: PAGE, DAVID L.
; APPLICANT: KING, MARY-CLAIRE
; APPLICANT: SZABO, CSILLA I.
; APPLICANT: JETTON, THOMAS L.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
; TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/603,753D
; FILING DATE: 20 FEB 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/373,799
; FILING DATE: 17 JAN 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11283
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens sapiens
```

```
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: normal and cancerous breast cells
CELL LINE: MCF-7
ORGANELLE: no
IMMEDIATE SOURCE:
LIBRARY: cDNA library derived from human
CLONE: obtained using published sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: BRCA2
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: gene encoding BRCA2 protein
PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
TITLE: susceptibility gene BRCA2
JOURNAL: Nature
VOLUME: 379
PAGES: 789-792
DATE: 1995
RELEVANT RESIDUES IN SEQ ID NO: 3
US-08-603-753D-3
Alignment Scores:
Pred. No.: 243 Length: 11283
Score: 67.00 Matches: 16
Percent Similarity: 51.11% Conservative: 7
Best Local Similarity: 35.56% Mismatches: 22
Query Match: 16.79% Indels: 0
DB: 2 Gaps: 0
US-09-092-296-15 (1-78) x US-08-603-753D-3 (1-11283)
QY 27 GlnLeuLysLeuLysSerPheLeuThrAsnSerSerTyrGluSerSerPheLeuGlu 46
Db 5055 AAATTATCATCTTAAGAGCTTAGGTGGCACACAGTCTCAATAGAAACAAGGTTTTTATCA 4996
QY 47 LeuLeuGluLysLeuLysLeuLeuLeuHisLeuProSerGlyThrSerValThrLeuHis 66
Db 4995 TTATTGAGAGAATTCTGCATCTTTACACTTTGGGCAGCTGTGATCTCAATGGTCTCA 4936
QY 67 HisalaArgSerGln 71
Db 4935 CATGCTAATTC AAGG 4921
RESULT 13
US-09-099-753-3/C
; Sequence 3, Application US/09099753
; Patent No. 6149903
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: PAGE, DAVID L.
; APPLICANT: KING, MARY-CLAIRE
; APPLICANT: SZABO, CSILLA I.
; APPLICANT: JETTON, THOMAS L.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
; TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
; CITY: DURHAM
```

STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,753
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,753
FILING DATE: 20 FEB 1996
APPLICATION NUMBER: U.S. 08/373,799
FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11283
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: gDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens sapiens
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: normal and cancerous breast cells
CELL LINE: MCF-7
ORGANELLE: no
IMMEDIATE SOURCE:
LIBRARY: cDNA library derived from human
CLONE: obtained using published sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: BRCA2
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: gene encoding BRCA2 protein
PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
SEQUENCE CHARACTERISTICS:
JOURNAL: Nature
VOLUME: 379
PAGES: 789-792
DATE: 1995
RELEVANT RESIDUES IN SEQ ID NO: 3
US-09-099-753-3
Alignment Scores:
Pred. No.: 243
Score: 67.00
Percent Similarity: 51.11%
Best Local Similarity: 35.56%
Query Match: 16.79%
DB: 3
Length: 11283
Matches: 16
Conservative: 7
Mismatches: 22
Indels: 0
Gaps: 0

US-09-092-296-15 (1-78) x US-09-099-753-3 (1-11283)
QY 27 GlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyrcLuserSerPheLeuGlu 46
DB 5055 AAATATACACCTTAAGAGCTTAGTGGCCACACAGCTCTCAATAGAACAAAGGTTTTATCA 4996
QY 47 LeuLeuGluLysLeuCysLeuLeuHisLeuProSerGlyThrSerValThrLeuHis 66
DB 4995 TTATTGAGAGATTCTGCATTTCTTTACACTTTGGGCGAGCTGTGATCTCAATGGTCTCA 4936
QY 67 HisAlaArgSerGln 71
DB 4935 CATGCTAATTCAGG 4921
RESULT 14
US-08-986-106-3/c
Sequence 3, Application US/08986106
Patent No. 6177410
GENERAL INFORMATION:
APPLICANT: HOLT, JEFFREY T.
APPLICANT: JENSEN, ROY A.
APPLICANT: KING, MARY-CLAIRE
APPLICANT: STEINER, MITCHELL S.
APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: THERAPEUTIC METHODS FOR
TITLE OF INVENTION: PROSTATE CANCER
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
STREET: BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,106
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,753
FILING DATE: 20 FEB 1996
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11283
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: BRCA2
PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
SEQUENCE CHARACTERISTICS:
JOURNAL: Nature
VOLUME: 379
PAGES: 789-792
DATE: 1995
US-08-986-106-3

```
Alignment Scores:
Pred. No.: 243 Length: 11283
Score: 67.00 Matches: 16
Percent Similarity: 51.11% Conservatives: 7
Best Local Similarity: 35.56% Mismatches: 22
Query Match: 16.79% Indels: 0
DB: 4 Gaps: 0

US-09-092-296-15 (1-78) x US-08-986-106-3 (1-11283)
QY 27 GlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyrGluSerSerPheLeuGlu 46
Db 5055 AAATTATCATTAAAGCTTAGTGGCCACACAGCTCTCAATAGAACAAAGGTTTTTATCA 4996
QY 47 LeuLeuGluLysLeuCysLeuLeuHisLeuProSerGlyThrSerValThrLeuHis 66
Db 4995 TTATTGAGAGAATTCGCAATTTCTTACACTTTGGGGCAGCTGTGATCTCAATGGTCTCA 4936
QY 67 HisAlaArgSerGln 71
Db 4935 CATGCTAATTCAGG 4921

RESULT 15
US-08-639-501-1/c
; Sequence 1, Application US/08639501
; Patent No. 5837492
; GENERAL INFORMATION:
; APPLICANT: Tavtligian, Sean V.
; APPLICANT: Kamb, Alexander
; APPLICANT: Sinard, Jacques
; APPLICANT: Couch, Fergus
; APPLICANT: Rommens, Johanna
; APPLICANT: Weber, Barbara
; TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1001
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,501
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/585,391
; FILING DATE: 11-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/576,559
; FILING DATE: 21-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/575,359
; FILING DATE: 20-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/573,779
; FILING DATE: 18-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-116802-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 229..10482
; US-08-639-501-1
Alignment Scores:
Pred. No.: 246 Length: 11385
Score: 67.00 Matches: 16
Percent Similarity: 51.11% Conservatives: 7
Best Local Similarity: 35.56% Mismatches: 22
Query Match: 16.79% Indels: 0
DB: 2 Gaps: 0

US-09-092-296-15 (1-78) x US-08-639-501-1 (1-11385)
QY 27 GlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyrGluSerSerPheLeuGlu 46
Db 5087 AAATTATCATTAAAGCTTAGTGGCCACACAGCTCTCAATAGAACAAAGGTTTTTATCA 5028
QY 47 LeuLeuGluLysLeuCysLeuLeuHisLeuProSerGlyThrSerValThrLeuHis 66
Db 5027 TTATTGAGAGAATTCGCAATTTCTTACACTTTGGGGCAGCTGTGATCTCAATGGTCTCA 4968
QY 67 HisAlaArgSerGln 71
Db 4967 CATGCTAATTCAGG 4953

Search completed: May 1, 2003, 06:05:50
Job time : 85 secs
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GenCore version 5.1.5
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2003, 05:17:21 ; Search time 1415 Seconds
(without alignments)
892.755 Million cell updates/sec

Title: US-09-092-296-15

Perfect score: 399

Sequence: 1 MGSLPLVLLTLTGSSRGTT.....SGTSVTLHARSQHVVVNCVT 78

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q=/cgn2_1/USPTO.spool/US09092296/runat_30042003_133103_14414/app.query.fasta_1.263
-DB=EST -QPM=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09092296.0CGN.1.1.1525 @runat_30042003_133103_14414 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_WRAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmv:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	399	100.0	456	12	BG506690 601861290
2	399	100.0	830	13	BI759796 603045679
3	394	98.7	449	10	AW293443 UI-H-B12-
4	381	95.5	422	12	BF002050 798c11.x
5	334	83.7	895	13	BI820029 603037210
6	307	76.9	865	13	BI820110 603037110
7	304	76.2	404	9	AI857998 wj69b01.x
8	208	52.1	552	17	AO718761 HS-5511_B
9	195.5	49.0	521	10	BB533837 BB533837
10	195.5	49.0	522	10	BB664284 BB664284
11	178	44.6	361	12	BF521842 UI-R-C2p-
12	156.5	39.2	328	9	AI136523 UI-R-C2p-
13	143	35.8	244	12	BF511043 UI-H-B14-
14	115	28.8	506	17	AZ241329 RPCI-23-7
15	115	28.8	633	17	AZ079350 RPCI-23-4
16	90	22.6	557	14	BQ552414 H4015F11-
17	85.5	21.4	338	13	BQ041163 BJ041163
18	85.5	21.4	374	13	BJ041184 BJ041184
19	85.5	21.4	397	13	BJ033159 BJ033159
20	85.5	21.4	402	13	BJ055543 BJ055543
21	85.5	21.4	644	13	BJ032429 BJ032429
22	85.5	21.4	685	13	BJ080213 BJ080213
23	82.5	20.7	260	13	BJ055523 BJ055523
24	82.5	20.7	613	10	BE53619 ur47h09.Y
25	81.5	20.4	504	10	BE191954 db85a04.x
26	81.5	20.4	608	13	BJ061093 BJ061093
27	80.5	20.2	329	13	BI312652 da125a09.
28	79.5	19.9	484	17	AZ367243 IM0116M18
29	79.5	19.9	623	9	AA543778 vk39e01.r
30	78	19.5	525	17	AQ360660 HS_5034.A
31	78	19.5	896	17	CNS0454L Tetraodon
32	78	19.5	1175	17	AG122004 Pan trogl
33	77	19.3	713	17	AQ349213 RPCI11-11
34	77	19.3	909	14	BQ957881 AGENCOURT
35	77	19.3	1129	12	BF101152 601754726
36	76.5	19.2	360	14	C62342 C62342 YuJ1
37	76.5	19.2	711	12	BG701480 602682714
38	76.5	19.2	729	13	BI551383 603192812
39	76.5	19.2	783	13	BI553452 603192812
40	76.5	19.2	816	13	BI753758 603028281
41	76.5	19.2	1001	17	CNS03FE9 Tetraodon
42	76.5	19.2	1054	13	BM547579 AGENCOURT
43	76	19.0	439	9	AA776143 ae89e12.s
44	76	19.0	576	13	BI359989 384782 MA
45	76	19.0	682	13	BJ140448 BJ140448

ALIGNMENTS

RESULT 1
BG506690 601861290F1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4070759 5'..
LOCUS mRNA sequence.
DEFINITION BG506690.1 GI:13468207
ACCESSION BG506690
VERSION BG506690.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 456)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC915 row: d column: 24
High quality sequence stop: 401.
Location/Qualifiers
1. .456
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4070759"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggcgctcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTAGCCGAGCGCGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

FEATURES
source

BASE COUNT 109 a 137 c 106 g 103 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 1.59e-37 Length: 456
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-09-092-296-15 (1-78) x BG506690 (1-456)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerHisGlyThr 20
DB 45 ATGGGGTCTGGGCTGGCCCTTGCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACA 104
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerTyr 40
DB 105 GGGCGGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 164
QY 41 GluSerPheLeuGluLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
DB 165 GAGTCCAGCTTCCTGGAATGCTTGAAGAGCTCTGCCCTCTCCATCTCCCTTCAGGG 224
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
DB 225 ACCAGCGTACCCCTCCACATGCAAGATCTCAACACCATGTGTCTGCAACACA 278

RESULT 2
BI759796

LOCUS BI759796 830 bp mRNA linear EST 25-SEP-2001
DEFINITION 603045679F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186107 5', mRNA sequence.
ACCESSION BI759796
VERSION BI759796.1 GI:15751374
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 830)
AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1464 row: m column: 20
High quality sequence stop: 432.
Location/Qualifiers
1. .830
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5186107"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colonies, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

FEATURES
source

BASE COUNT 175 a 276 c 210 g 168 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 3.59e-37 Length: 830
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-092-296-15 (1-78) x BI759796 (1-830)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerHisGlyThr 20
DB 81 ATGGGGTCTGGGCTGGCCCTTGCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACA 140
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerTyr 40
DB 141 GGACCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 200
QY 41 GluSerPheLeuGluLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
DB 201 GAGTCCAGCTTCCTGGAATGCTTGAAGAGCTCTGCCCTCTCCATCTCCCTTCAGGG 260
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
DB 261 ACCAGCGTACCCCTCCACATGCAAGATCTCAACACCATGTGTCTGCAACACA 314

RESULT 3
AW293443/c

LOCUS AW293443 449 bp mRNA linear EST 16-JAN-2000
DEFINITION UT-H-BI2-alm-c-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:272182 3', mRNA sequence.
ACCESSION AW293443
VERSION AW293443.1 GI:6700079
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 449)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbrrp/image/image.html
Seq primer: M13 Forward
POLYA=yes.

FEATURES
source

Location/Qualifiers
1. .449
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2727182"
/clone_lib="NCI-CGAP-Sub4"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; The
NCI-CGAP-Sub4 library is a subtracted library derived from
the NCI-CGAP-Sub2 library which is a subtracted library
derived from the NCI-CGAP-Sub1 library, which is a
subtracted library derived from BI. BI constitutes a
mixture of 21 normalized or subtracted NCI-CGAP
libraries: NCI-CGAP-Co4, NCI-CGAP-Pr22, NCI-CGAP-Pr28,
NCI-CGAP-Co10, NCI-CGAP-Co16, NCI-CGAP-Kid5,
NCI-CGAP-Kid12, NCI-CGAP-Kid3, NCI-CGAP-Kid11,
NCI-CGAP-LyM2, NCI-CGAP-Br2, NCI-CGAP-Co8, NCI-CGAP-CLL1,
NCI-CGAP-Le12, NCI-CGAP-Brn23, NCI-CGAP-Lu5,
NCI-CGAP-Lu24, NCI-CGAP-Lu19, NCI-CGAP-GC4, NCI-CGAP-GC6,
NCI-CGAP-Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below
NCI-CGAP-Kid3 pool 1 : LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE CloneIDs 1322376-1323911,
1456008-1456775, 1500552-1502855) NCI-CGAP-Kid5 pool 1 :
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs
1323912-1325831, 1471368-1472903, 1492104-1493255)
NCI-CGAP-Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE
CloneIDs 1414920-1417991, 1520904-1522439) NCI-CGAP-GC4
pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743
) NCI-CGAP-Pr22 pool 1 : LLAM 2457-2459, 2758-2759,
3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959,
1217928-1220615) NCI-CGAP-Co10 pool 1 : LLAM 2644-2653,
2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351)
) Subtraction was performed as previously described
[Bonaldi, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
Genome Research 6, 791-806.]
TAG_LIB=NCI-CGAP-Co4
TAG_TISSUE=colon
TAG_SEQ=CTTCG

BASE COUNT 104 a 108 c 134 g 103 t
ORIGIN

Alignment Scores:
Pred. No.: 6.09e-37 Length: 449
Score: 394.00 Matches: 77
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.72% Mismatches: 0
Query Match: 98.75% Indels: 0
DB: 10 Gaps: 0

US-09-092-296-15 (1-78) x AW293443 (1-449)

Qy 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
|||||

Db 387 ATGGGGTCTGGGCTGCCCTTGTCTCTCTTGGCAGCTCACATGGAACA 328
Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerTyr 40
|||||
Db 327 GGGCGGGATGACTTTCGAAGTGAAGGAGTCTTTTCGACACAGTTCCCTCTAT 268
Qy 41 GluSerSerPheLeuGlnLeuLeuGluLysLeuLysLeuLeuHisLeuProSerGly 60
|||||
Db 267 GAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTGCCTCCCTCCATCTCCCTTCAGGG 208
Qy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
|||||
Db 207 ACCAGCGTCACCTCCACCATGCAAGATCTCACACCATGTTGTCTGCAACACA 154

RESULT 4

BF002050/c
LOCUS BF002050 422 bp mRNA linear EST 06-OCT-2000
DEFINITION 7498c11.x1 NCI-CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314516 3',
mRNA sequence.

ACCESSION BF002050
VERSION BF002050.1 GI:10702325
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 422)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov

Seq primer: -40UP from Gbco.

FEATURES

Location/Qualifiers
1. .422
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3314516"
/clone_lib="NCI-CGAP_Co16"
/tissue_type="colon tumor, RER-"
/lab_host="DH10B"
/note="Organ: colon; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not 1; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP_Co10 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldi. "

BASE COUNT 102 a 99 c 130 g 88 t
ORIGIN

Alignment Scores:
Pred. No.: 1.96e-35 Length: 422
Score: 381.00 Matches: 77
Percent Similarity: 97.47% Conservative: 0
Best Local Similarity: 97.47% Mismatches: 1
Query Match: 95.49% Indels: 1
DB: 12 Gaps: 0

US-09-092-296-15 (1-78) x BF002050 (1-422)

Qy 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
|||||

```

|||||
Db 377 ATGGGGTCTGGGCTGCCCTTGCTCTCTGACCCCTCGCTGGCAGCTCACATGGACA 318
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
|||||
Db 317 GGGCGGGTATGACATTTGCAACTGAAGCTGAAGGAGTCTTTCTTGACAAATTCCTCTAT 258
QY 41 GluSerSerPheLeuGluLeuLeuGlu-LysLeuCysLeuLeuLeuHisLeuProSerG1 60
|||||
Db 257 GAGTCCAGCTTCCTGGAATGCTTGAAAAGNTNGCTCCTCCTCATCTCCTTCAGG 198
QY 60 YThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
|||||
Db 197 GACCGGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 143

RESULT 5
BI820029 895 bp mRNA linear EST 04-OCT-2001
LOCUS 603037210F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178171 5',
DEFINITION mRNA sequence.
ACCESSION BI820029
VERSION BI820029.1 GI:15931579
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 895)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rcgapsb@email.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Cloning Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11444 row: c column: 04
High quality sequence start: 5
High quality sequence stop: 422.
Location/Qualifiers
1..895
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5178171"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SpOxT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

BASE COUNT 349 a 229 c 202 g 115 t
ORIGIN

Alignment Scores:
Pred. No.: 2,08e-29 Length: 895
Score: 334.00 Matches: 64
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.71% Indels: 0
DB: 13 Gaps: 0

US-09-092-296-15 (1-78) x BI820029 (1-895)

```

```

QY 15 GlySerSerHisGlyThrGlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPhe 34
|||||
Db 13 GGAGCTCACATGGGAACAGCGCGGTATGACTTGGCAACTGAAGCTGAAGGAGTCTTTT 72
QY 35 LeuThrAsnSerSerTyrGluSerSerPheLeuGluLeuLeuLysLeuCysLeuLeu 54
Db 73 CTGACAAATTCCTCTATGAGTCCAGCTTCCTGGAATGCTTGAAAAGCTCTGCCTCCTC 132
QY 55 LeuHisLeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisVal 74
Db 133 CTCATCTCTCCTTCAGGACGAGTCCACCTCCACCATGCAAGATCTCAACACCATGTT 192
QY 75 ValCysAsnThr 78
|||||
Db 193 GTCTGCAACACA 204

RESULT 6
BI820110 865 bp mRNA linear EST 04-OCT-2001
LOCUS 603037110F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178170 5',
DEFINITION mRNA sequence.
ACCESSION BI820110
VERSION BI820110.1 GI:15931660
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 865)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rcgapsb@email.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Cloning Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11444 row: c column: 03
High quality sequence stop: 417.
Location/Qualifiers
1..865
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5178170"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SpOxT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

BASE COUNT 330 a 219 c 198 g 117 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 3.19e-26 Length: 865
Score: 307.00 Matches: 63
Percent Similarity: 98.44% Conservative: 0
Best Local Similarity: 98.44% Mismatches: 1
Query Match: 76.94% Indels: 1
DB: 13 Gaps: 0

US-09-092-296-15 (1-78) x BI820110 (1-865)

```

QY	15	GlySerSerHisGlyThrGlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPhe	34
DB	13	GGAGCTCACAGGACAGGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTT	72
QY	35	LeuThrAsnSerSerTyrGluSerPheLeuGluLeuLysLeuGluLysLeuCysLeuLeu	54
DB	73	CTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATG-CTTGAAAGCTGCTGCTCCTC	131
QY	55	LeuHisLeuProSerGlyThrSerValThrLeuHisAlaArgSerGlnHisHisVal	74
DB	132	CTCCATCTCCCTTCAGGACACGCTCCCTCCACCATCCAGATCTCACACCACTT	191
QY	75	ValCysAsnThr	78
DB	192	GTCTGCAACACA	203
RESULT 7			
LOCUS	AI857998	404 bp mRNA linear	EST 21-DEC-1999
DEFINITION	*J169D01.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408041	3',	
ACCESSION	AI857998		
VERSION	AI857998.1	GI:5511614	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 404)		
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/hcicgap .		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgaps-remail.nih.gov		
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.		
	cDNA Library Preparation: M. Bento Soares, Ph.D.		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html		
	Insert length: 629 Std Error: 0.00		
	Seq primer: 400P from Gibco		
	High quality sequence stop: 395.		
FEATURES	Location/Qualifiers		
source	1..404		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2408041"		
	/clone_lib="NCI_CGAP_Lu19"		
	/tissue_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and metastatic)"		
	/dev_stage="adult"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	97 a 105 c 117 g 84 t	1 others	
ORIGIN			
Alignment Scores:			
Pred. No.:	2.57e-26	Length:	404
Score:	304.00	Matches:	59
Percent similarity:	95.24%	Conservative:	1

Best Local Similarity:	93.65%	Mismatches:	3
Query Match:	76.19%	Indels:	0
DB:	9	Gaps:	0
US-09-092-296-15 (1-78) x AI857998 (1-404)			
QY	16	SerSerHisGlyThrGlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeu	35
DB	324	ACTCTCGATCCGACGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTG	265
QY	36	ThrAsnSerSerTyrGluSerPheLeuGluLeuLysLeuGluLysLeuCysLeuLeu	55
DB	264	ACAAATCTCTATGAGTCCAGCTTCTGGAATGCTTGAAAGCTTGGCTCCTCCTC	205
QY	56	HisLeuProSerGlyThrSerValThrLeuHisAlaArgSerGlnHisHisVal	75
DB	204	CATCTCCCTTCAGGACACGCTCCCTCCACCATCCAGATCTCAACACCATGTTGTC	145
QY	76	CysAsnThr	78
DB	144	TGCAACACA	136
RESULT 8			
LOCUS	AQ718761	552 bp DNA linear	GSS 13-JUL-1999
DEFINITION	HS.5511.B2.F09.T7A RPCI-11 Human Male BAC library Homo sapiens genomic clone Plate=1087 Col=18 Row=L, DNA sequence.		
ACCESSION	AQ718761		
VERSION	AQ718761.1	GI:5468077	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 552)		
JOURNAL	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Kellier,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.		
MEDLINE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome		
COMMENT	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589		
	Contact: Mahairas GG, Wallace JC, Hood L		
	High Throughput Sequencing Center		
	University of Washington		
	401 Queen Anne Avenue North, Seattle, WA 98109, USA		
	Tel: (206) 616-3618		
	Fax: (206) 616-3887		
	Email: jwallace@u.washington.edu		
	Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.husc.washington.edu		
	Plate: 1087 row: L column: 18		
	Seq primer: T7		
	Class: BAC ends		
	High quality sequence stop: 552.		
FEATURES	Location/Qualifiers		
source	1..552		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="Plate=1087 Col=18 Row=L"		
	/clone_lib="RPCI-11 Human Male BAC Library"		
	/sex="male"		
	/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"		
BASE COUNT	141 a 153 c 124 g 117 t	17 others	
ORIGIN			

[illegible]

/clone="UI-R-C2p-nq-e-02-0-UI"
/clone_lib="UI-R-C2p"
/dev_stage="adult"

/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography.
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996)"

BASE COUNT 79 a 121 c 91 g 70 t
ORIGIN

Alignment Scores:

Pred. No.: 2.02e-11 Length: 361
Score: 178.00 Matches: 38
Percent Similarity: 65.79% Conservative: 12
Best Local Similarity: 50.00% Mismatches: 26
Query Match: 44.61% Indels: 0
DB: 12 Gaps: 0

US-09-092-296-15 (1-78) x BF521842 (1-361)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 22 ATGGAGCCCTTCAGTGCCTCTCTCCCTCGACCTCTCGACCTACTCGAAGG 81
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 82 CCAACAAAGGTGACTTTTGCAAGTAAACTGACCGAGGCATCTCAGGCCAAGACCTCCCA 141
QY 41 GluSerSerPheLeuGluLeuGluLysLeuCysLeuLeuHisValSerGly 60
Db 142 GACTCGGCTTCTGGACATGCTCCAAAGATCTGCTCTCTCCACTCTCACCAGG 201
QY 61 ThrSerValThrLeuHisAlaArgSerGlnHisHisValValCys 76
Db 202 ACCAATGTACCTTCATCATAAAGGGCCACACACACCTTACCTGC 249

RESULT 12

LOCUS A1136523 328 bp mRNA linear EST 11-FEB-1999
DEFINITION UI-R-C2p-nq-e-02-0-UI.s1 UI-R-C2p Rattus norvegicus cDNA clone
VERSION A1136523
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 328)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL
MEDLINE
COMMENT

Genome Res. 6 (9), 791-806 (1996)
97044477

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence tag present in the cDNA between the NotI site and the
oligo-dT track served to identify it as a clone from the normalized
adult lung library. cDNA library Preparation: M. Fatima Bonaldo,
Ph.D. Clone distribution: clones will be available through Research
Genetics

Seq primer: M13 Forward.

FEATURES
source

Location/Qualifiers
1..328
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C2p-nq-e-02-0-UI"
/clone_lib="UI-R-C2p"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography.
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996)"

BASE COUNT 62 a 77 c 98 g 91 t
ORIGIN

Alignment Scores:

Pred. No.: 6.33e-09 Length: 328
Score: 156.50 Matches: 30
Percent Similarity: 71.93% Conservative: 11
Best Local Similarity: 52.63% Mismatches: 15
Query Match: 39.22% Indels: 1
DB: 9 Gaps: 1

US-09-092-296-15 (1-78) x A1136523 (1-328)

QY 21 GlyPro---GlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSer 39
Db 313 GGGCCCAACAAGGTGACTTTGCAAGTAAACTGACCGAGGCATCTCAGGCCAAGACCTCC 254
QY 40 TyrGluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuHisValValCys 59
Db 253 CAAGACTCCGCTTTTGGACATGCTCCAAAGATCTGCTCTCTCTCCACTCTCACC 194
QY 60 GlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCys 76
Db 193 GGGACCAATGTACCTTCATCATATAAGGGCCACACACCTTACCTGC 143

RESULT 13


```

Db      341  AACTCCAGTGCTCTGGACATGCTCCAAAAGGTAGTTTTTAGTAGCCGGATAGCAGTGGT  282
Qy      50  -----
Db      281  ACTGCACGGCTTCTCTGGGTGCCTGCAGGTCTCTCTCTGGGGCTGGCTGACTGGACACAGG  222
Qy      51  -----LeuCysLeuLe 54
                        : : : : :
Db      221  AGTGGGTACCATCTTACACCTCATCTCTGGGATCATTTATGTACCCAGATCTGCCTCT  162
Qy      54  uLeuHisLeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisVa  74
                        : : : : :
Db      161  CCTCCATCTGCCATCAGGGACCANTGTACCCCTCTTTCACAAAGGACCACACACTACCT  102
Qy      74  lValCys 76
                        : : :
Db      101  TACTTGC 95

```

RESULT 15	AZ079350	633 bp	DNA	linear	GSS 31-MAR-2000
LOCUS	AZ079350/c				
DEFINITION	RPCI-23-438H19.TV RPCI-23 Mus musculus genomic clone RPCI-23-438H19 sequence.				
ACCESSION	AZ079350				
VERSION	AZ079350				
KEYWORDS	GI:7372249				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 633)				
AUTHORS	Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Kroi, M., de Jong, P. and Fraser, C.M.				
TITLE	Mouse BAC End Sequences from Library RPCI-23				
JOURNAL	Unpublished (1999)				
COMMENT	Other_GSSs: RPCI-23-438H19.TJ Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pietre de Jong (pietred@jeng.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 438 row: H column: 19 Seq primer: T7 Class: BAC ends.				

```

class: BAC ends.
Location/Qualifiers
1. .633
  /organism="Mus musculus"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="RPCI-23-438H19"
  /clone_lib="RPCI-23"
  /sex="Female"
  /lab_host="DH10B"
  /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
  EcoRI; Site_2: EcoRI; female C57BL/6J mouse kidney and/or
  brain genomic DNA was isolated and partially digested
  with a combination of EcoRI and EcoRI Methylase. Size
  selected DNA was cloned into the pBACe3.6 vector at the
  EcoRI sites. The ligation products were transformed into
  DH10B electrocompetent cells (BRL Life Technologies)."
138 a 191 c 161 g 143 t

```

```

Pred. No.: 0.00131          Length: 633
Score: 115.00             Matches: 31
Percent Similarity: 40.78%   Conservative: 11
Best Local Similarity: 30.10% Mismatches: 14
Query Match: 28.82%         Indels: 47
DB: 17                     Gaps: 1

US-09-092-296-15 (1-78) x AZ079350 (1-633)

Qy 21 GlyProGlyMetThrLeuGlnLeuLySLeuLySGLuSerPheLeuThrAsnSerSerrYr 40
    GGGG :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 401 GGGCAAAGGTGACTTTGAGGTAAAGCTCAGCGAGACTTTTCAGGACAAGACCTCCGAC 342
    :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::

Qy 41 GluSerPheLeuGluLeuLeuGluLyS- - - - - 50
    :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 341 AACTCCAGTGCTCTGGACATGCTCCAAAAGGTAGTTTTAGTAGGGGATAGCAGTGGT 282
    :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::

Qy 50 - - - - - 50
Db 281 ACTGCACAGCTTCTGGGTGGCTCGAGGTCTCTGCTGGGGCTGGGTGAGTGAGCAGGG 222
Qy 51 - - - - - 51
    - - - - - LeuCysLeuLe 54
    :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 221 AGTGGGTGACCATCTTAGACCTCATCTCGGATCATTAATAATAACACAGATCTGCCTCT 162
    :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::

Qy 54 uLeuHisLeuProSerGlyThrSerValThrLeuHisHisIalaArgSerGlnHisHisIa 74
    :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 161 CCTCCATCTGCCATCAGGACCATTGTACCCCTCTTCACAAAGGACCACCACACTACCT 102
    :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::

Qy 74 lValCys 76
    : |||
Db 101 TACTGTG 95

Search completed: May 1, 2003, 06:04:16
Job time : 1420 secs

```

GenCore version 5.1.5
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2003, 05:14:32 ; Search time 218 Seconds
(without alignments)
805.761 Million cell updates/sec

Title: US-09-092-296-15

Perfect score: 399

Sequence: 1 MGSGLPLVLLTLGSSHG.....SGTSVTLHARSQHVVVCNT 78

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+pn.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool/US09092296/runat_30042003_133102_14392/app_query.fasta_1.263
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO_XLPYX -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
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18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	399	100.0	422	21	AAZ65087	Membrane-bound pro
2	399	100.0	422	21	AAZ65087	Human DNA encoding
3	399	100.0	422	22	AAF92090	Human PRO1098 CDNA
4	399	100.0	422	22	AAF92090	Human PRO1098 CDNA
5	399	100.0	431	21	AAZ98124	Human signal pepti
6	399	100.0	439	20	AAV84366	Human stomach carc
7	349	87.5	624	24	ABK81818	DNA representing 1
8	161.5	40.5	729	23	AAZ65519	DNA encoding novel
9	75	18.8	715	22	AAH70861	Human cervical can
10	75	18.8	1248	23	ABL20661	Drosophila melanog
11	75	18.8	3323	23	ABL20660	Drosophila melanog
12	73	18.3	23580	22	AAZ85556	Genomic sequence #
13	73	18.3	23580	22	AAZ85556	Human immune/haema
14	73	18.3	23580	22	AAZ85556	Human osteoblast d
15	73	18.3	23580	22	AAZ85556	Human cDNA differe
16	72.5	18.2	785	21	AAA72675	plastidial phospho
17	72.5	18.2	1733	20	AAZ59149	Pea mutant plastid
18	72.5	18.2	1875	20	AAZ59146	Pea wild-type plas
19	72.5	18.2	2006	20	AAZ59147	Pea mutant plastid
20	72.5	18.2	2182	19	AAV00731	Pea plastidial pho
21	71	17.8	1571	24	ABL90445	Human polynucleoti
22	71	17.8	1650	21	AAZ97083	Human secreted pro
23	71	17.8	1853	21	AAZ97083	Human membrane-ass
24	71	17.8	1949	22	AAH25763	Oesophagus cancer
25	71	17.8	1952	24	ABK49215	cDNA encoding huma
26	71	17.8	1970	21	AAZ67344	Human ORF ORF1899
27	70.5	17.7	1668	23	ABL22127	Drosophila melanog
28	70.5	17.7	3905	23	ABL22126	Drosophila melanog
29	70	17.5	874	21	AAH75583	Human ORF ORF2138
30	70	17.5	2545	22	AAH75583	Human cDNA sequenc
31	70	17.5	13485	22	AAZ31469	Human DNA for a no
32	70	17.5	13485	22	ABK44039	Genomic DNA encodi
33	70	17.5	13485	22	ABK44039	Human polynucleoti
34	69	17.3	2094	23	AAZ78887	DNA encoding novel
35	69	17.3	2406	21	AAA09590	Human phosphodiast
36	69	17.3	3631	22	ABA03665	Human PDE10A CDNA
37	69	17.3	4576	21	AAA09589	Human phosphodiast
38	69	17.3	11809	22	ABA21072	Human nervous syst
39	69	17.3	11809	22	ABA21072	Human reproductiv
40	68.5	17.2	9751	22	AAZ18386	Recombinant viral
41	68.5	17.2	9751	24	ABL60796	FIV-Oma3 recombin
42	68.5	17.2	23474	23	AAZ59511	Propionibacterium
43	68.5	17.2	26997	22	AAZ59511	Tumour suppressor
44	68	17.0	2554	21	AAZ36963	DNA encoding a hum
45	68	17.0	2798	21	AAZ36964	DNA encoding a hum

ALIGNMENTS

RESULT 1	
AAZ65087	
ID	AAZ65087 standard; cDNA; 422 BP.
XX	
AC	AAZ65087;
XX	
DT	05-APR-2000 (first entry)
XX	
DE	Membrane-bound protein PRO1098 encoding cDNA.
XX	
KW	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW	pharmaceutical; receptor immunoadhesin; gene mapping; ss.
OS	Homo sapiens.
XX	
PN	WO9963088-A2.
XX	
PD	09-DEC-1999.

XX 02-JUN-1999; 99WO-US12252.
PF 02-JUN-1998; 98US-0087607.
XX 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
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PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 18-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090451.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.

PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
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PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
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PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 02-JUL-1998; 98US-0091678.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
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PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
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PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.

(GETH) GENENTECH INC.

XX Baker K, Chen J, Goddard A, Smith V, Watanabe CK;
XX Wood WI, Yuan J;
XX WPI; 2000-072883/06.

DR P-PSDB; AAY66741.
XX Membrane-bound proteins and related nucleotide sequences -
PT Claim 2; Fig 257; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Alignment Scores:
Pred. No.: 1-55e-43 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

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QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuGlySerHisGlyThr 20
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Db 58 ATGGGTCTGGCTGGCTGCTCTCTCTGACCTCTCTGCGAGTCACATGGAACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLeuGlySerPheLeuThrAsnSerSerTyr 40
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Db 118 GGCCCGGTATGACTTTCACACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuLeuGluLeuLeuGlySerGlnHisValCysAsnThr 60
|||||
Db 178 GAGTCAGCTCTCTGGAATGTGTTGAAAAGCTCTGCTCTCTCTCCATCTCCCTTCAGGG 237
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisValValCysAsnThr 78
|||||
Db 238 ACCGCGTCACCTCCACCATGCAAGATCTCACACCATGTTGTCTGCAACACA 291

RESULT 2
AAS46045
ID AAS46045 standard; cDNA; 422 BP.
XX
XX AAS46045;
AC
XX
XX 18-DEC-2001 (first entry)
DE
XX Human DNA encoding PRO polypeptide sequence #121.
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.
XX

PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05641.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
DR P-PSDB; AAU29144.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -
XX
XX Claim 2; Fig 241; 774pp; English.
XX
XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX
XX Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;
SQ

Alignment Scores:		1.55e-43	Length:	422
Pred. No.:		399.00	Matches:	78
Score:		100.00%	Conservative:	0
Percent Similarity:		100.00%	Mismatches:	0
Best Local Similarity:		100.00%	Indels:	0
Query Match:		100.00%	Gaps:	0
DB:		22		
US-09-092-296-15 (1-78) x AAS46045 (1-422)				
Qy	1	MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20		
Db	58	ATGGGGTCGGGCTGCCCTTGCTCTTGACCTCTGGCAGCTCACAATGGAAACA 117		
Qy	21	GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40		
Db	118	GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCTAT 177		
Qy	41	GluSerSerPheLeuGluLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60		
Db	178	GAGTCCAGCTTCTTGGAAATGCTTGAAGAAGCTTGCCTCTCTCCATCTCCCTCAGGG 237		
Qy	61	ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78		
Db	238	ACCAGGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291		
RESULT 3				
AAF92090				
ID	AAF92090	standard; cDNA; 422 BP.		
XX	AC	AAF92090;		
XX	DT	15-MAY-2001 (first entry)		
XX	DE	Human PRO1098 cDNA.		
XX	KW	Human; PRO protein; mapping; ss.		
XX	OS	Homo sapiens.		
XX	PN	WO200116318-A2.		
XX	PD	08-MAR-2001.		
XX	PF	24-AUG-2000; 2000WO-US23328.		
XX	PR	01-SEP-1999; 99WO-US20111.		
XX	PR	15-SEP-1999; 99WO-US21090.		
XX	PR	07-DEC-1999; 99US-0169495.		
XX	PR	09-DEC-1999; 99US-0170262.		
XX	PR	11-JAN-2000; 2000US-0175481.		
XX	PR	18-FEB-2000; 2000WO-US04341.		
XX	PR	22-FEB-2000; 2000WO-US04414.		
XX	PR	01-MAR-2000; 2000WO-US05601.		
XX	PR	03-MAR-2000; 2000US-0187202.		
XX	PR	25-APR-2000; 2000US-0199397.		
XX	PR	22-MAY-2000; 2000WO-US14042.		
XX	PR	05-JUN-2000; 2000US-0209832.		
XX	PA	(GETH) GENENTECH INC.		
XX	PI	Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;		
XX	PI	Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;		
XX	XX			
XX	DR	WPI: 2001-183260/18.		
XX	DR	P-PSDB; AAB87558.		
XX	PT	Eighty four nucleic acids encoding PRO polypeptides, useful in		
XX	PT	molecular biology, including use as hybridization probes, and in		
XX	PT	chromosome and gene mapping.		
XX	PS	Claim 2; Fig 65; 278pp; English.		

XX	The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.			
SQ	Sequence	422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;		
Alignment Scores:				
Pred. No.:	1.55e-43	Length:	422	
Score:	399.00	Matches:	78	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	22	Gaps:	0	
US-09-092-296-15 (1-78) x AAF92090 (1-422)				
Qy	1	MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20		
Db	58	ATGGGGTCGGGCTGCCCTTGCTCTTGACCTCTGGCAGCTCACAATGGAAACA 117		
Qy	21	GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40		
Db	118	GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCTAT 177		
Qy	41	GluSerSerPheLeuGluLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60		
Db	178	GAGTCCAGCTTCTTGGAAATGCTTGAAGAAGCTTGCCTCTCTCCATCTCCCTCAGGG 237		
Qy	61	ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78		
Db	238	ACCAGGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291		
RESULT 4				
AAF44233				
ID	AAF44233	standard; cDNA; 422 BP.		
XX	AC	AAF44233;		
XX	DT	02-APR-2001 (first entry)		
XX	DE	Human PRO1098 (UNQ541) nucleotide sequence SEQ ID NO:362.		
XX	KW	Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing; diagnostic assay; ss.		
XX	OS	Homo sapiens.		
XX	PN	WO200073454-A1.		
XX	PD	07-DEC-2000.		
XX	PF	30-MAR-2000; 2000WO-US08439.		
XX	PR	02-JUN-1999; 99WO-US12252.		
XX	PR	23-JUN-1999; 99US-0141037.		
XX	PR	07-JUL-1999; 99US-0143048.		
XX	PR	20-JUL-1999; 99US-0144758.		
XX	PR	26-JUL-1999; 99US-0145698.		
XX	PR	28-JUL-1999; 99US-0146222.		
XX	PR	17-AUG-1999; 99US-0149396.		
XX	PR	15-SEP-1999; 99WO-US21090.		
XX	PR	15-SEP-1999; 99WO-US21547.		
XX	PR	08-OCT-1999; 99US-0158663.		
XX	PR	30-NOV-1999; 99WO-US28313.		
XX	PR	01-DEC-1999; 99WO-US28301.		

PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoletti NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI; 2001-032160/04.
 DR P-PSDB; AAB65264.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 2; Fig 257; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Alignment Scores:
 Pred. No.: 1.55e-43 Length: 422
 Score: 399.00 Matches: 78
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-092-296-15 (1-78) x AAF44233 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuLeuLeuGlySerHisGlyThr 20
 |||||
 DB 58 ATGGGCTGCGGCTGCGCCCTTGCTCTCTCTGACCTCTCTGGCAGCTCACATGACCA 117
 |||||
 QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
 |||||
 DB 118 GGGCCGGGTATGACTTGGCACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTAT 177
 |||||
 QY 41 GlnSerSerPheLeuLeuLeuLeuLeuGluLysLeuLysLeuLeuHisLeuProSerGly 60
 |||||
 DB 178 GAGTCAGCTTCTGGATGCTTGTGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTAGG 237
 |||||
 QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
 |||||
 DB 238 ACCAGGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTTCTGCAACACA 291
 |||||

RESULT 5
 AAZ98124
 ID AAZ98124 standard; cDNA; 431 BP.
 XX
 AC AAZ98124;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE Human signal peptide containing protein HSPP-16 cDNA SEQ ID NO:150.
 XX
 DE Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's disease; ovulatory defect;
 KW muscular dystrophy; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14484.
 XX
 PR 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX
 PA (INCYTE) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone CA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 DR WPI; 2000-160673/14.
 DR P-PSDB; AAY87239.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease -
 XX
 PS Claim 9; Page 261; 327pp; English.
 XX
 CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
 CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities and can
 CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPP. Antagonists of
 CC HSPP are used to treat or prevent disorders associated with increased
 CC activity or function of HSPP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
 CC nucleic acids can be used for the recombinant production of HSPP, for
 CC detecting HSPP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPP
 CC from natural sources.
 XX

SQ Sequence 431 BP; 93 A; 135 C; 101 G; 102 T; 0 other;

Alignment Scores:

Pred. No.: 1.6e-43 Length: 431
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-092-296-15 (1-78) x AAZ98124 (1-431)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
DB 51 ATGGGGTCTGGGCTGCCCTTGCTCTCTTGACCTCTTGACCTGCGAGCTCACATGGAACA 110
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
DB 111 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 170
QY 41 GluSerSerPheLeuGluLeuLeuGluLysLeuLysLeuLeuLeuLeuLeuProSerGly 60
DB 171 GAGTCCAGCTTCTCGAATTCCTTGAAGAGCTCTGCCTCTCTCCATCTCCCTTCAGGG 230
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
DB 231 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTGTGCAACACA 284

RESULT 6

AAV84366
ID AAV84366 standard; cDNA to mRNA; 439 BP.

XX AC AAV84366;

XX 30-MAR-1999 (first entry)

XX Human stomach carcinoma cDNA clone HP10408.

XX Transmembrane protein; HP10408; human; stomach cancer; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 75..311

XX /tag= a

XX /note= "cDNA comprising the coding region (minus

XX the stop codon) is claimed (Claim 3)"

XX W09855508-A2.

XX 10-DEC-1998.

XX 03-JUN-1998; 98WO-JP02445.

XX 03-JUN-1997; 97JP-014948.

XX (PROT-) PROTEGENE INC.

XX (SAGA) SAGAMI CHEM RES CENTRE.

XX Kato S, Sekine S, Yamaguchi T;

XX WPI; 1999-045730/04.

XX P-PSDB; AAW88498.

XX New human proteins containing transmembrane domains and their

XX encoding sequences - useful in the preparation of antibodies and

XX large-scale protein production, gene diagnosis, and gene therapy

XX Claim 4; Page 135; 178pp; English.

XX This is the nucleotide sequence of cDNA clone HP10408, which

XX includes a coding region (also claimed) for a novel human

XX transmembrane protein (see AAW88498). The clone was isolated from a

CC stomach cancer cDNA library using a signal sequence detection
CC method, and by protein synthesis by in vitro translation. The
CC encoded protein has a putative signal sequence and a putative
CC internal transmembrane domain. The invention provides nucleotide
CC sequences (see AAV84359-76) coding for 18 transmembrane proteins
CC (see AAW88491-508), vectors containing such polynucleotides, and
CC eukaryotic cells containing the vectors. The proteins can be
CC used as antigens or as compositions in the preparation of
CC antibodies against the proteins. The polynucleotides can be used
CC as probes for gene diagnosis, and as gene sources for gene therapy
CC and large-scale production of proteins encoded by the cDNA. The
CC host cells are used for the detection of ligands corresponding to
CC the expressed proteins, and the screening of low mol.wt. medicines.
XX SQ Sequence 439 BP; 89 A; 137 C; 109 G; 104 T; 0 other;

Alignment Scores:

Pred. No.: 1.64e-43 Length: 439
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-092-296-15 (1-78) x AAV84366 (1-439)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuLeuGlySerSerHisGlyThr 20
DB 75 ATGGGTCTGGGCTGCCCTTGCTCTCTTGACCTCTTGACCTGCGAGCTCACATGGAACA 134

QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
DB 135 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 194

QY 41 GluSerSerPheLeuGluLeuLeuGluLysLeuLysLeuLeuLeuLeuLeuProSerGly 60
DB 195 GAGTCCAGCTTCTCGAATTCCTTGAAGAGCTCTGCCTCTCTCCATCTCCCTTCAGGG 254

QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
DB 255 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTGTGCAACACA 308

RESULT 7

ABK81818
ID ABK81818 standard; DNA; 624 BP.

XX AC ABK81818;

XX 13-AUG-2002 (first entry)

XX DNA representing lung specific gene #4.

XX Lung specific gene; gene therapy; vaccine; lung cancer;

XX cancer staging; cancer monitoring; cancer diagnosis;

XX imaging lung cancer; metastases; gene; ss.

XX Homo sapiens.

XX WO200218576-A2.

XX 07-MAR-2002.

XX 27-AUG-2001; 2001WO-US26684.

XX 28-AUG-2000; 2000US-228378P.

XX (DIAD-) DIADEXUS INC.

XX Chen S, Macina RA, Sun Y, Recipon H;

XX WPI; 2002-434904/46.

XX New lung specific genes and their encoded proteins, useful in gene

PT therapy or as a vaccine for treating lung cancer, as well as for
PT measuring metastases of lung cancer, or staging, monitoring, diagnosing
XX or imaging lung cancer -
XX
PS Claim 1: Page 161; 206pp; English.
XX
CC The invention describes a new lung specific gene and it's variants. The
CC lung specific gene proteins and genes are useful in gene therapy or as a
CC vaccine for treating lung cancer. Lung specific genes are also useful for
CC staging, monitoring, diagnosing or imaging lung cancer, as well as for
CC measuring metastases of lung cancer. This sequence represents a lung
CC specific gene described in the invention.
XX
SQ Sequence 624 BP; 129 A; 175 C; 182 G; 138 T; 0 other;

Alignment Scores:
Pred. No.: 1.13e-36 Length: 624
Score: 349.00 Matches: 78
Percent Similarity: 49.37% Conservative: 0
Best Local Similarity: 49.37% Mismatches: 0
Query Match: 87.47% Indels: 80
DB: 24 Gaps: 1

US-09-092-296-15 (1-78) x ABR81818 (1-624)

Qy 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 16 ATGGGTCTGGGCTGCCCCCTTGTCTCTCTGTGACCTCTCTGGCAGCTCAGTGAACA 75
Qy 20 ----- 20
Db 76 GGTGAGGGCTAGAGGGCAGGACTCTCTGGTCCCTGTGCAAGAGAGCCAGAAAAAGG 135
Qy 20 ----- 20
Db 136 GGTGGGACTTATGCTCCCTGAGAGTGACAGACAGACACCCAGCTCTGAGTTCACAGAG 195
Qy 20 ----- 20
Db 196 CTCTGAGGGGCAATTGCTGGGGAAGAGGAAGTGTGCGGGGAGCGTGAGCAGGAAGTTC 255
Qy 20 ----- 20
Db 256 TGTGCTCCGGAGGAATCAGCCCTGACTGCTGGTCTCTAAAGTGTACTTGTGGATCGCA 315
Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 316 GGGCCGGGTATGACTTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTAT 375
Qy 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuLeuHisLeuProSerGly 60
Db 376 GAGTCCAGCTTCTGGGAATGCTTGAAGAGCTGCGCTCTCTCTCCCTTCAGGG 435
Qy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 436 ACCAGGGTCACCTCCACCATGCAAGATCTCAACACCATGTTGCTGTGCAACACA 489

RESULT 8
AA565519
ID AA565519 standard; cDNA; 729 BP.
XX
AC AA565519;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #1323.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS Homo sapiens.
XX
PN W0200175067-A2.

XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US08631.
PF
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
PA
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG01332.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 1323; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 729 BP; 187 A; 169 C; 152 G; 146 T; 75 other;

Alignment Scores:
Pred. No.: 9.77e-12 Length: 729
Score: 161.50 Matches: 37
Percent Similarity: 66.07% Conservative: 0
Best Local Similarity: 66.07% Mismatches: 2
Query Match: 40.48% Indels: 17
DB: 23 Gaps: 1

US-09-092-296-15 (1-78) x AAS65519 (1-729)

Qy 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 25 ATGGGTCTGGGCTGCCCCCTTGTCTCTCTGACCTCTCTGGCAGCTCAGTGAACA 84
Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGlu----- 32
Db 85 GGACCGGGGTATGACTTTTGCAACTGAGAGCTGAGGGGGTCAAGAGACACAGGCTTC 144
Qy 33 -----SerPheLeuThrAsnSerSer 39
Db 145 AATGGGTGCATTTCAAGGAAGTCACTTCTCTCTTAACATAAGCAGC 192
RESULT 9
AAH70861/c
ID AAH70861 standard; cDNA; 715 BP.
XX
AC AAH70861;

```
XX 19-SEP-2001 (first entry)
XX Human cervical cancer marker nucleic acid 2135.
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX Homo sapiens.
XX WO200142467-A2.
XX 14-JUN-2001.
XX 08-DEC-2000; 2000WO-US33312.
XX 08-DEC-1999; 90US-0169681.
XX 21-DEC-1999; 90US-0171350.
XX 14-MAR-2000; 2000US-0189315.
XX 12-MAY-2000; 2000US-0203791.
XX 09-JUN-2000; 2000US-0210600.
XX 21-JUL-2000; 2000US-0220114.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Deeds J, Berger A, Zhao X;
XX WPI; 2001-375006/39.
XX New isolated nucleic acid for diagnosing and treating cervical cancer
XX and for assessing and detecting compounds for treating the cancer -
XX Claim 1; Page 451-452; 1051pp; English.
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
XX cervical cancer with cytostatic activity. The nucleic acids and encoded
XX polypeptides are useful: to assess if a patient is afflicted with
XX cervical cancer or has a pre-malignant condition; to monitor the
XX progression of cervical cancer or a premalignant condition in a patient;
XX and to select and/or assess the efficacy of a compound or therapy for
XX inhibiting cervical cancer in a patient. The nucleic acids may also be
XX useful for gene therapy.
XX Sequence 715 BP; 247 A; 151 C; 138 G; 179 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 2.73 Length: 715
XX Score: 75.00 Matches: 23
XX Percent Similarity: 53.03% Conservative: 12
XX Best Local Similarity: 34.85% Mismatches: 25
XX Query Match: 18.80% Indels: 6
XX DB: 22 Gaps: 2
XX
XX US-09-092-296-15 (1-78) x AAH70861 (1-715)
XX
XX QY 6 ProLeuValLeuLeuLeuLeuLeuGlySerSerHisGlyThrGlyProGlyMetThr 25
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 594 CCCTAGTACCGGCGCGCAGTTTGTGGAATTCGCCTTCGAACGGCGCGGAGGTA 535
XX
XX QY 26 LeuGluLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyGluSerSerPheLeu 45
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 534 CTATCTCTAAGTAAATTAAGTATTAGGCTTCAATCTGAGATAGCTTGCCACATT 475
XX
XX QY 46 GluLeuLeuGluLysLeuCys-----LeuLeuLeuHisLeuProSerGly 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 474 GAGTTAATACATGAGATTTCTATTCTCTGGAAGTACTGAATATATATCTGTCGAAGT--- 418
XX
XX QY 61 ThrSerValThrLeuHis 66
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 417 TGCAGCATACCATCCAT 400
XX
XX RESULT 10
XX ABL20661/c
XX ID ABL20661 standard; DNA; 1248 BP.
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```
XX ABL20661;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 13456.
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX Drosophila melanogaster.
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX Claim 1; SEQ ID NO 13456; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABLI6176-ABLI30511), expressed DNA
XX sequences (ABLI01840-ABLI6175) and the encoded proteins
XX (ABBS7737-ABBS72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 1248 BP; 285 A; 375 C; 335 G; 253 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 6.02 Length: 1248
XX Score: 75.00 Matches: 25
XX Percent Similarity: 47.37% Conservative: 11
XX Best Local Similarity: 32.89% Mismatches: 30
XX Query Match: 18.80% Indels: 10
XX DB: 23 Gaps: 3
XX
XX US-09-092-296-15 (1-78) x ABL20661 (1-1248)
XX
XX QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuLeuThrLeu---LeuGlySerSerHisGly 19
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 753 CTGGGCTGGGCGCTGAGCCTGTGCTGCCTGCCTGAGCTGCTGCTGGCTGAGCTGGGC 694
XX
XX QY 20 ThrGlyProGlyMetThrLeuGluLeuLysLeuLysGluSerPheLeuThrAsnSerSer 39
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 693 CTGGGATTTGATTGTTGATTTCACCTGACCTGCTGTTAGGTGCTAGCTGAGCTCGG 634
XX
XX QY 40 TyrGluSerSerPheLeuLeuLeuGluLeuGluLysLeuCysLeuLeuLeuProSer 59
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 633 TATGATTCGGGC-----TGTCCACGAGCTGCTGCATCTTCATCAAGACGG 586
XX
XX QY 60 GlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValVal 75
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 585 AGCACCATACGCTCCAT-----CATCATATGCTGC 553
XX
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PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0223237.
PR 14-SEP-2000; 2000US-0223238.
PR 14-SEP-2000; 2000US-0223239.
PR 14-SEP-2000; 2000US-0223240.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
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PR 27-SEP-2000; 2000US-0235834.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
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PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
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PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
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PR 08-NOV-2000; 2000US-0246609.
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PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
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PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.

PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
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PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
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PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2000US-0254097.
PR 05-JAN-2001; 2000US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPT; 2001-476224/51.
XX Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the respiratory system including respiratory
PT cancers and also for testing and detection e.g. diagnosis -
XX
XX Disclosure; SED ID No 990; 546pp; English.
XX The present invention relates to the isolation of novel human
CC respiratory antigens (AAU17685-AAU17975), and cDNA and genomic
CC sequences encoding for these polypeptides. The sequences of the
CC invention are useful for preventing, treating and/or prognosing
CC disorders related to the respiratory system including throat
CC disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis),
CC lung disorders (e.g. pneumonia, allergic disorders e.g. asthma,
CC pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of
CC the respiratory tissues e.g. lung cancer. The polynucleotide sequences
CC of the invention are useful in gene therapy and antisense therapy.
CC AAS28161-AAS28764 represent genomic sequences encoding for novel
CC human respiratory antigens.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 23580 BP; 5938 A; 5961 C; 5927 G; 5754 T; 0 other;

Alignment Scores:
Pred. No.: 712 Length: 23580
Score: 73.00 Matches: 29
Percent Similarity: 44.71% Conservative: 9
Best Local Similarity: 34.12% Mismatches: 23
Query Match: 18.30% Indels: 24
DB: 22 Gaps: 5

US-09-092-296-15 (1-78) x AAS28556 (1-23580)

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Db 17157 GGTTCCTCGAAGTTCTCACTTTGCTGAGTCAGGCTGACCTGGAGAACCTGCATCT 17216
Qy 21 GlyPro-----GlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThr 36
Db 17217 GGGCCATGAGACATCTTGGGGGATGACTTTCAACCTTCAGATGAAGAGAGGT----- 17270
Qy 37 AsnSerSerTyrGluSerSerPheLeuGluLeuGluLeuGluLeuLeuHis 56
Db 17271 -----CTAGAGAGCTGTTGCTTCTTCACTCT 17297
Qy 57 LeuProSerGlyThrSerValThrLeuHisHisAla-----ArgSerGlnHisHis 73
Db 17298 GATCCAATGGGGAGTCA---ACCAGGCACCGGGCTCAATCAACAGCAATAAATCATCAC 17354

QY 74 ValValCysAsnThr 78
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Db 17355 TGTCTGAGTCAACT 17369
RESULT 13
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ID AAK87248 standard; DNA; 23580 BP.
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AC AAK87248;
XX
DT 07-NOV-2001 (first entry)
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DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42060.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
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PR 11-JUL-2000; 2000US-0217487.
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PR 01-SEP-2000; 2000US-0229287.
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PR 08-SEP-2000; 2000US-0231242.
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PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
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PR 25-SEP-2000; 2000US-0234998.
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PR 08-NOV-2000; 2000US-0246524.
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PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
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PR 17-NOV-2000; 2000US-0249208.
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PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249297.

PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Disclosure; SEQ ID NO 42060; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 23580 BP; 5938 A; 5961 C; 5927 G; 5754 T; 0 other;

Alignment Scores:
Pred. No.: 712 Length: 23580
Score: 73.00 Matches: 29
Percent Similarity: 44.71% Conservative: 9
Best Local Similarity: 34.12% Mismatches: 23
Query Match: 18.30% Indels: 24
DB: 22 Gaps: 5

US-09-092-296-15 (1-78) x AAK87248 (1-23580)

QY 4 GlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThr----- 20
Db 17157 GGTTCCTCGAAGTTCTACTTGTCTGAGTCAGGCTGACCTTGAGGAACCCCTGACATCT 17216
QY 21 GlyPro-----GlyMetThrLeuGlnLeuLeuLeuLeuLeuLeuLeuLeuHis 36
Db 17217 GGGCCATGAGACATCTTGGGGGATGACTTTCAACCTTCAGATGAAGACGAGGT----- 17270
QY 37 AsnSerSerTyrGluSerSerPheLeuGluLeuLeuGluLeuLeuLeuLeuHis 56
Db 17271 -----CTAGAGAAGGTGTGCTTCTCACTCT 17297
QY 57 LeuProSerGlyThrSerValThrLeuHisHisAla-----ArgSerGlnHisHis 73
Db 17298 GATCCAATGGGGAGTCA---ACCGAGCACCGGGCTCAATCAACAGCAATAAATCATCAC 17354

QY 74 ValValCysAsnThr 78
Db 17355 TGTCGAGGTCAACT 17369
RESULT 14
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ID ABQ88164 standard; cDNA; 86080 BP.
XX ABQ88164;
XX
XX 18-SEP-2002 (first entry)
XX Human osteoblast differentiation related cDNA SEQ ID NO 71.
KW Human; osteoblast; stem cell differentiation; bone tissue deposition;
KW osteoporosis; osteopathic; ss.
XX Homo sapiens.
XX
XX WO200250301-A2.
XX
XX 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-US48276.
XX
XX 18-DEC-2000; 2000US-255882P.
XX 24-APR-2001; 2001US-285691P.
XX (GENE-) GENE LOGIC INC.
XX (PROC) PROCTER & GAMBLE CO.
XX Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
XX Mertz L;
XX WPI; 2002-557663/59.
XX Use of genes and their expression profiles associated with osteoblast
XX differentiation for screening modulators bone formation, for diagnosing
XX or treating e.g. osteoporosis, or as markers for the differentiation
XX process -
XX Claim 1; SEQ ID NO 71; 78pp + Sequence Listing; English.
XX The invention relates to genes and their expression profiles are used
XX for:
XX (a) screening modulators of precursor stem cell differentiation into
XX osteoblasts, or bone tissue deposition;
XX (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
XX osteoblast formation or osteoporosis; or
XX (c) treating or monitoring treatment of the conditions cited in (b), or
XX monitoring the progression of bone tissue deposition.
XX Specific conditions include postmenopausal osteoporosis, glucocorticoid
XX osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
XX drug-induced abnormalities in bone formation or bone loss, conditions
XX that involve altered bone metabolism (e.g. idiopathic juvenile
XX osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
XX Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
XX osteoblast differentiation associated cDNA marker of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 86080 BP; 21583 A; 21475 C; 21694 G; 21328 T; 0 other;

Alignment Scores:
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Score: 73.00 Matches: 29
Percent Similarity: 44.71% Conservative: 9
Best Local Similarity: 34.12% Mismatches: 23
Query Match: 18.30% Indels: 24
DB: 22 Gaps: 5

GenCore version 5.1.5
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 1, 2003, 05:14:56 ; Search time 1151 Seconds

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1972.214 Million cell updates/sec

Title: US-09-092-296-15

Perfect score: 399

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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21: em_or:*
22: em_ov:*
23: em_pat:*
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41: em_htgo_other:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	399	100.0	422	6	AX376174	Sequence
3	399	100.0	422	6	AX403475	Sequence
4	394	98.7	484	9	AY102070	Homo sapi
5	349	87.5	624	6	AX472955	Sequence
6	317	79.4	47323	9	AC005937	Homo sapi
7	317	79.4	104154	2	AL773541	Homo sapi
8	317	79.4	156272	9	AL669830	Human DNA
9	317	79.4	178688	2	AL713893	Homo sapi
10	317	79.4	192650	9	AB023048	Homo sapi
11	317	79.4	200000	9	AP000511	Homo sapi
12	312	78.2	84474	9	AL662854	Human DNA
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14	203	50.9	34980	6	AX344554	Sequence
15	121	30.3	132977	2	RN510020	Sequence
16	109.5	27.4	175345	2	AC022301	Mus muscu
17	106	26.6	349980	6	AX344571	Sequence
18	99.5	24.9	337832	2	AC099175	Rattus no
19	90	22.6	201296	10	AC115299	Mus muscu
20	85.5	21.4	149078	2	AC117264	Oryza sat
21	83.5	20.9	176233	2	AC102885	Mus muscu
22	83.5	20.9	196980	2	AC122405	Mus muscu
23	82.5	20.7	185078	2	AC097616	Rattus no
24	82	20.6	96445	9	AC107397	Homo sapi
25	81.5	20.4	2182	10	BC019813	Mus muscu
26	80	20.1	168426	2	AC124357	Mus muscu
27	80	20.1	189175	2	AC121200	Rattus no
28	79.5	19.9	169241	2	AC129409	Rattus no
29	79.5	19.9	206168	10	AL672307	Mouse DNA
30	79	19.8	109238	9	AC004997	Homo sapi
31	79	19.8	158257	9	AC005585	Homo sapi
32	79	19.8	169281	2	AC098927	Rattus no
33	79	19.8	172811	2	AC103034	Rattus no
34	79	19.8	191111	2	AC114527	Rattus no
35	78.5	19.7	225924	2	AC074210	Mus muscu
36	78	19.5	11078	1	AE009918	Pyrobacul
37	78	19.5	171602	2	AC130212	Mus muscu
38	78	19.5	193567	2	AC102127	Mus muscu
39	77.5	19.4	165402	2	AC128392	Rattus no
40	77.5	19.4	178676	2	AC087868	Mus muscu
41	77.5	19.4	226903	2	AC079272	Mus muscu
42	77	19.3	64607	9	AC005021	Homo sapi
43	77	19.3	172478	2	AC015844	Homo sapi
44	77	19.3	176630	2	AC109427	Rattus no
45	77	19.3	203827	10	AL669816	Mouse DNA

ALIGNMENTS

AX092334
LOCUS AX092334 422 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 65 from Patent WO0116318.
ACCESSION AX092334
VERSION AX092334.1 GI:13444481
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 422)
Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 65 08-MAR-2001;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
1..422
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN
Alignment Scores:
Pred. No.: 3.84e-42 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-092-296-15 (1-78) x AX092334 (1-422)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
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Db 58 ATGGGCTCTGGGCTGGCCCTTGCTCTGACCTCTTGGCAGCTCAGTGGACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
|||||
Db 118 GGGCCGGTATGACTTTCGAACCTGAAGCTGGAAGAGCTTTCTGACAAATTCCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuGluLysLeuLysLeuLeuHisValValCysAsnThr 60
|||||
Db 178 GAGTCCAGCTTCTGGAATTCCTGAAAGCTGCTGCTCTCTCCATCTGCTGCAACA 237
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
|||||
Db 238 ACCAGGTCACCTCCACATGCAAGATCTCAACACCATGTTGCTGCAACA 291
RESULT 2
AX376174
LOCUS AX376174 422 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 241 from Patent WO0168848.
ACCESSION AX376174
VERSION AX376174.1 GI:19170479
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 241 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
1..422
/organism="Homo sapiens"

/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN
Alignment Scores:
Pred. No.: 3.84e-42 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-092-296-15 (1-78) x AX376174 (1-422)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
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Db 58 ATGGGCTCTGGGCTGGCCCTTGCTCTGACCTCTTGGCAGCTCAGTGGACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
|||||
Db 118 GGGCCGGTATGACTTTCGAACCTGAAGCTGGAAGAGCTTTCTGACAAATTCCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuGluLysLeuLysLeuLeuHisValValCysAsnThr 60
|||||
Db 178 GAGTCCAGCTTCTGGAATTCCTGAAAGCTGCTGCTCTCTCCATCTGCTGCAACA 237
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
|||||
Db 238 ACCAGGTCACCTCCACATGCAAGATCTCAACACCATGTTGCTGCAACA 291
RESULT 3
AX403475
LOCUS AX403475 422 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 362 from Patent WO0073454.
ACCESSION AX403475
VERSION AX403475.1 GI:21436973
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 362 07-DEC-2000;
Genentech Inc. (US)
FEATURES
source Location/Qualifiers
1..422
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN
Alignment Scores:
Pred. No.: 3.84e-42 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-092-296-15 (1-78) x AX403475 (1-422)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
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Db 58 ATGGGCTCTGGGCTGGCCCTTGCTCTGACCTCTTGGCAGCTCAGTGGACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
|||||
Db 118 GGGCCGGTATGACTTTCGAACCTGAAGCTGGAAGAGCTTTCTGACAAATTCCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuGluLysLeuLysLeuLeuHisValValCysAsnThr 60
|||||
Db 178 GAGTCCAGCTTCTGGAATTCCTGAAAGCTGCTGCTCTCTCCATCTGCTGCAACA 237
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
|||||
Db 238 ACCAGGTCACCTCCACATGCAAGATCTCAACACCATGTTGCTGCAACA 291
RESULT 3
AX403475
LOCUS AX403475 422 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 362 from Patent WO0073454.
ACCESSION AX403475
VERSION AX403475.1 GI:21436973
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 362 07-DEC-2000;
Genentech Inc. (US)
FEATURES
source Location/Qualifiers
1..422
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN
Alignment Scores:
Pred. No.: 3.84e-42 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-092-296-15 (1-78) x AX403475 (1-422)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
|||||
Db 58 ATGGGCTCTGGGCTGGCCCTTGCTCTGACCTCTTGGCAGCTCAGTGGACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
|||||

|||||
Db 118 GGGCGGGTATGACTTCAACTGAAGCTGAAGGAGTCTTTCTGCAAAATTCCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
|||||
Db 178 GAGTCCAGCTTCTGGAATCTGTGAAAGCTCTGCCCTCCCTCCATCTCCCTTCAGGG 237
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
|||||
Db 238 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGTGTGTCGCAACACA 291
RESULT 4
AY102070
LOCUS AY102070 484 bp mRNA linear PRI 18-JUN-2002
DEFINITION Homo sapiens surfactant associated protein G mRNA, partial
sequence.
ACCESSION AY102070
VERSION AY102070.1 GI:21464498
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 484)
AUTHORS Walker M.G. and Spiro, P.
JOURNAL Genes co-expressed with pulmonary surfactants
REFERENCE 2 (bases 1 to 484)
AUTHORS Walker M.G. and Spiro, P.
JOURNAL Direct Submission
TITLE Submitted (07-MAY-2002) Incyte Genomics, 1475 Flamingo Way,
Sunnyvale, CA 94087-3405, USA
FEATURES
source
1..484
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="236582"
gene <1..>484
/gene="surfactant associated protein G"
/note="SFTPG"
BASE COUNT 124 a 149 c 110 g 101 t
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Alignment Scores:
Pred. No.: 1.99e-41 Length: 484
Score: 394.00 Matches: 77
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.72% Mismatches: 0
Query Match: 98.75% Indels: 0
Gaps: 0
DB:
US-09-092-296-15 (1-78) x AY102070 (1-484)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
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Db 55 ATGGGGTCTGGGCTGCCCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 114
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
|||||
Db 115 GGGCGGGTATGACTTCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 174
QY 41 GluSerSerPheLeuGluLeuGluLysLeuCysLeuLeuHisLeuHisLeuProSerGly 60
|||||
Db 175 GAGTCCAGCTTCTGGAATCTGTGAAAGCTCTGCCCTCCCTCCATCTCCCTTCAGGG 234
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
|||||
Db 235 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGTGTGTCGCAACACA 288
RESULT 5
AX472955
LOCUS AX472955 624 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 4 from Patent WO0218576.

AX472955
VERSION AX472955.1 GI:22207742
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Chen, S.Y., Macina, R.A., Sun, Y. and Recipon, H.
JOURNAL Compositions and methods relating to lung specific genes
Patent: WO 0218576-A 4 07-MAR-2002;
Diadexus, Inc. (US)
FEATURES
source
1..624
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 129 a 175 c 182 g 138 t
ORIGIN
Alignment Scores:
Pred. No.: 1.61e-35 Length: 624
Score: 349.00 Matches: 78
Percent Similarity: 49.37% Conservative: 0
Best Local Similarity: 49.37% Mismatches: 0
Query Match: 87.47% Indels: 80
Gaps: 1
DB:
US-09-092-296-15 (1-78) x AX472955 (1-624)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
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Db 16 ATGGGGTCTGGGCTGCCCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 75
QY 20 ----- 20
Db 76 GGTGAGGCTAGAGGCGGAGGACTCTGGGTCTCTGTGCAAGAGAGGAGGAGGAGG 135
QY 20 ----- 20
Db 136 GGTGGAGCTTCATGTCT 195
QY 20 ----- 20
Db 196 CTCTGGAGGGGCAATTTGGGGAAGAGAACTGTCCCGGGGAGCGGTGACAGGAGGTT 255
QY 20 ----- 20
Db 256 TGTGTCTCCGGAGGAATCAGCCCTGACTGCTGGGTCTCTAAAGCTGTACTTCTGGATCC 315
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
|||||
Db 316 GGGCGGGTATGACTTTCACCTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 375
QY 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuHisLeuProSerGly 60
|||||
Db 376 GAGTCAGCTTCTCGGAATTTGCTTGAAGAGCTCTGCTCTCTCTCTCTCTCTCTCT 435
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
|||||
Db 436 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGTGTCTGCAACACA 489
RESULT 6
AC005937
LOCUS AC005937 47323 bp DNA linear PRI 05-NOV-1998
DEFINITION Homo sapiens clone UWGC:370M23.002 from 6p21, complete sequence.
ACCESSION AC005937
VERSION AC005937.1 GI:3845393
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 47323)

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Db 68088 CTCCTTCAGGACGAGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGC 68147
QY 77 AsnThr 78
|||||
Db 68148 AACACA 68153
RESULT 8
AL669830/c
LOCUS Human DNA sequence from clone XXbac-118E17 on chromosome 6,
DEFINITION complete sequence.
ACCESSION AL669830
VERSION AL669830.9 GI:20135762
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Johnson, C.
Direct Submission
Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 10, 2002 this sequence version replaced gi:20067510.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep XXbac-118E17 is
from a CHORI-501 human bac - PGF cell line library VECTOR:
PTARBAC2.1
This sequence was generated from part of bacterial clone contigs
constructed by the MHC Haplotype Consortium and collaborators.
Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6/MHC.
FEATURES
source
1. .156272
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-118E17"
/clone_lib="CHORI-501"
BASE COUNT 41135 a 37989 c 36907 g 40241 t
ORIGIN
Alignment Scores:
Pred. No.: 1.52e-28 Length: 156272
Score: 317.00 Matches: 78
Percent Similarity: 38.61% Conservative: 0
Best Local Similarity: 38.61% Mismatches: 0
Query Match: 79.45% Indels: 124
DB: Gaps: 2
US-09-092-296-15 (1-78) x AL669830 (1-156272)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
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Db 25856 ATGGGGCTGGGCTGCCCTTGCTCTCTTGACCCCTCTTGSCAGCTCACATGGAACA 25797

QY 20 ----- 20
Db 25796 GGTGAGGGCTAGAGGGCAGGACTCCTGGGTCCCTGTGGCAAGAGAGCCAGAGAAAGG 25737
QY 20 ----- 20
Db 25736 GGTGGGACTTCATGGTCCCTGAGAGTGACAGAGACACCCAGCTCTCGAGCTTCCAAGAGG 25677
QY 20 ----- 20
Db 25676 CTCTGGAGGGCAATGCTGGGGAGAGGAAGTGTCCGGGGAGCGGTGAGCAGGAAGGTTTC 25617
QY 20 ----- 20
Db 25616 TGTGTCTCGGAGGAATCAGCCCTGACTGCTGGGTCTAAGCTGTACTTCTGGATCCGCA 25557
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
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Db 25556 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTAT 25497
QY 41 GluSerSerPheLeuLeuGluLys----- 50
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Db 25496 GAGTCAGGCTTCTCGAATGCTTGAAAGAGTAGTCTTTTGGAGGGGAAAGATGGGGCT 25437
QY 50 ----- 50
Db 25436 GTGTGTTGTGAGTCAGTTTGGGCTCTGCTGGGTCTGAGTCTCTCCGTGGTGGGAATG 25377
QY 51 -----LeuCysLeuLeuLeuHis 56
|||||
Db 25376 GAGAGCTCTTACATGGCGCCCTTTAACCCCTTGTGCCAGCTCTGCTCCTCCTCAT 25317
QY 57 LeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCys 76
|||||
Db 25316 CTCCTCTCAGGAGCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTGTCTGC 25257
QY 77 AsnThr 78
|||||
Db 25256 AACACA 25251
RESULT 9
AL713893
LOCUS Homo sapiens chromosome 6 clone XXbac-307M4, *** SEQUENCING IN
DEFINITION PROGRESS ***, 6 unordered pieces.
ACCESSION AL713893
VERSION AL713893.5 GI:19847952
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Sims, S.
Direct Submission
Submitted (26-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 29, 2002 this sequence version replaced gi:19772907.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: bpg307M4
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 177277 bases at least Q40
Consensus quality: 177708 bases at least Q30
Consensus quality: 177956 bases at least Q20

Insert size: 178188; sum-of-contigs
 Insert size: 192613; 0.9% error; agarose-1p
 Quality coverage: 8.57x in Q20 bases; sum-of-contigs Quality
 coverage: 8.00x in Q20 bases; agarose-1p

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 6 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.

1 37410: contig of 37410 bp in length
 * 37411 37510: gap of 100 bp
 * 37511 82372: contig of 44862 bp in length
 * 82373 82472: gap of 100 bp
 * 82473 142457: contig of 59985 bp in length
 * 142458 142557: gap of 100 bp
 * 142558 152859: contig of 10302 bp in length
 * 152860 152959: gap of 100 bp
 * 152960 172054: contig of 19095 bp in length
 * 172055 172154: gap of 100 bp
 * 172155 178688: contig of 6534 bp in length.

FEATURES

source

1. 178688
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="Xbac-307M4"
 /clone_lib="CHORI-501"
 1. 37410

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/note="assembly_fragment:03218
 fragment_chain:1"

misc_feature

37511..82372
 /note="assembly_fragment:00918
 fragment_chain:1"

misc_feature

82473..142457
 /note="assembly_fragment:03231
 fragment_chain:1"

misc_feature

142558..152859
 /note="assembly_fragment:03008
 fragment_chain:1"

misc_feature

152960..172054
 /note="assembly_fragment:04309
 fragment_chain:1"

misc_feature

172155..178688
 /note="assembly_fragment:03507
 fragment_chain:1"

clone_end:r7
 vector_side:right

BASE COUNT 46316 a 40707 c 42166 g 48998 t 501 others
 ORIGIN

Alignment Scores:

Pred. No.: 179e-28 Length: 178688
 Score: 317.00 Matches: 78
 Percent Similarity: 38.61% Conservative: 0
 Best Local Similarity: 38.61% Mismatches: 0
 Query Match: 79.45% Indels: 124
 DB: 2 Gaps: 2

US-09-092-296-15 (1-78) x AL713893 (1-178688)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuGlySerSerHisGlyThr 20

Db 173497 ATGGGGTCGTGGGCGCCCTGTGCTCTTGGACCTCTCTGCGAGCTCACATGAACA 173556

QY 20 ----- 20

Db 173557 GGTGAGGGCTAGAGGGCAGGACTCTGGGTCTGCGAAGAGAGCCAGACAAAGG 173616

QY 20 ----- 20

Db 173617 GGTGGGACTTCATGGTCCCTGAGAGTGACAGAGACACCCCGAGCTCTGAGCTTCCAAGAGG 173676
 QY 20 ----- 20
 Db 173677 CTCTGGAGGGGCATTGCTGGGGAAGAGAACTGTGCCGGGAGCGTGAGCAGAGGTTTC 173736
 QY 20 ----- 20
 Db 173737 TGTGTCTCCGGAGGAATCAGCCCTGACTCCTGGGTCTTAAGCTGTACTTCTGGATCCGCA 173796
 QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
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 Db 173797 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCAT 173856
 QY 41 GluSerSerPheLeuGlnLeuLys----- 50
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 Db 173857 GAGTCACAGCTTCTGGAATTTGCTTGAAGAGTAGTTCTTTGGAAGGGGNAAGATGGGCT 173916
 QY 50 ----- 50
 Db 173917 GTCTGTTTGTGAGTCAGTTTGGCCCTCTGCTGGGTCTGTGGATGTCTCCGTGGGAATG 173976
 QY 51 -----LeuCysLeuLeuHis 56
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 Db 173977 GAGAGCTCTTACATGGCGCCCTTTAACCCCTTTGTTCCAGCTCTGCTCTCTCAT 174036
 QY 57 LeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValLys 76
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 Db 174037 CTCCCTTCAGGAGCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGC 174096
 QY 77 AsnThr 78
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Db 174097 AACACA 174102

RESULT 10

AB023048

LOCUS

DEFINITION

AB023048

ACCESSION

AB023048

VERSION

AB023048.1

KEYWORDS

HTG

SOURCE

Homo sapiens

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p21.3"
 /clone="53L9"
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 Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
 clone:53L9, complete sequence.

AB023048

HTG

AB023048.1 GI:5672603

Homo sapiens

Homo sapiens cell_line:978SK DNA, clone:53L9.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (sites)

Shiina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,

Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,

Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,

Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,

Bahram,S. and Inoko,H.

Molecular dynamics of MHC genesis unraveled by sequence analysis of

The I.796,938-bp HLA class I region

Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)

20027539

2 (bases 1 to 192650)

Direct Submission

Shiina,T. and Takishima,N.

Submitted (29-JAN-1999) Takashi Shiina, Tokai University School of

Medicine, Department of Molecular Life Science 2; Bohseidai,

Isehara, Kanagawa 259-1193, Japan

(E-mail:tshina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,

Fax:81-463-94-8884)

Location/Qualifiers

1. 192650

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/map="6p21.3"

/clone="53L9"

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Score: 317.00 Matches: 78				
Percent Similarity: 38.61% Conservative: 0				
Best Local Similarity: 38.61% Mismatches: 0				
Query Match: 79.45% Indels: 124				
DB: 9 Gaps: 2				
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QY	41	GlusSerPheLeuGluLeuLeuLys-----	50	
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QY	57	LeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCys	76	
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QY	77	AsnThr	78	
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DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				

REFERENCE	2	(bases 1 to 200000)	
AUTHORS	Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-SEP-1999) Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491, Fax:81-3-5214-8470)		
COMMENT	This sequence is conducted by Tokai University as a JST sequencing Team.		
FEATURES	Principal Investigator: Hidetoshi Inoko Ph.D Phone:+81-463-93-1121, Fax:+81-463-94-8884, The sequence is submitted by Human Genome Sequencing in ALIS project of JST Japan Science and Technology Corporation (JST) 5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan For further information about this sequences, please visit our sequence archive web site (http://www-alis.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alis.tokyo.jst.go.jp.		
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QY 50 ----- 50
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QY 57 LeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCys 76
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RESULT 12
AL662854/c

LOCUS
DEFINITION
Homo sapiens
Human DNA sequence from clone XXbac-105N19 on chromosome 6,
complete sequence.

ACCESSION
AL662854
VERSION
AL662854.7 GI:20068660
KEYWORDS
HTG
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Tracey, A.
Direct Submission
Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requesters: clonerequest@sanger.ac.uk
On Apr 7, 2002 this sequence version replaced gi:19031750.
During difference assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: En: EMBL, Sw:
SWISSPROT, Tr: TrEMBL, Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C.elegans/wormpep XXbac-105N19 is
from a CHORI-502 human bac - COX cell line library VECTOR:
PTABAC2.1
This sequence was generated from part of bacterial clone contigs
constructed by the MHC Haplotype Consortium and collaborators.
Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6/MHC.
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Query Match: 78.20% Indels: 124
DB: Gaps: 2

US-09-092-296-15 (1-78) x AL662854 (1-84474)

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QY 51 -----LeuCysLeuLeuLeuHis 56
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RESULT 13
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LOCUS
DEFINITION
Sequence 4 from Patent WO0200932.
ACCESSION
AX344553
VERSION
AX344553.1 GI:18492439
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synthetic construct.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
Diagnosis of known genetic parameters within the mhc
Patent: WO 0200932-A 4 03-JAN-2002;
Epigenomics AG (DE)
FEATURES
Location/Qualifiers
source
1. .349980

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Score:          203.00      Matches:      55
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Best Local Similarity: 27.50%      Mismatches:  9
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DB:             6          Gaps:       2

US-09-092-296-15 (1-78) x AX344553 (1-349980)

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Qy  21 ----- 21

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Qy  21 ----- 21

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Qy  21 ----- 21

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Qy  22 -----Pro 22
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Qy  43  SerPheLeuGluLeuLeuGluLys----- 50
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Qy  50 ----- 50

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Qy  51 -----LeuCysLeuLeuLeuHisLeuPro 58
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Db 319325 TCTCTTACATAACGCCCTTTAAACCCCTTTATTTCCCAACTCTACCTCTCTCCATCTCCCT 319266

Qy  59  SerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
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RESULT 14
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DEFINITION Sequence 5 from Patent W00200932.
ACCESSION  AX344554
VERSION    AX344554.1  GI:18492440
KEYWORDS   .
SOURCE     synthetic construct.
ORGANISM   synthetic construct.
REFERENCE  1
AUTHORS    Olek, A., Piepenbrock, C. and Berlin, K.
TITLE      Diagnosis of known genetic parameters within the mhc
JOURNAL    Patent: WO 0200932-A 5 03-JAN-2002;
Epigenomics AG (DE)
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            /notes="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-Original length of seq 2: 3.673778 <223>-split as follows.-seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 2.749.980-seq 23 2.700.001 3.049.980-seq 24 3.000.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.673.778"

BASE COUNT      92349 a  5068 c  82248 g 170315 t
ORIGIN

Alignment Scores:
Pred. No.:      1,71e-13      Length:      349980
Score:          203.00      Matches:      55
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DB:             6          Gaps:       2

US-09-092-296-15 (1-78) x AX344554 (1-349980)

Qy  3  SerGlyLeuProLeuValLeuLeuThrLeuGlySerSerHisGlyThrGly--- 21
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Db 19805 TCTAAACTACCCCTTATCCCTCTTAAACCTCTTAAACAACCTCACATAAAACAAATAAA 19746

Qy  21 ----- 21

Db 19745 AACTAAAAACAACAACTCCTTAATCCCTATACAAAAAACCACCAAAAAAATAAA 19686

Qy  21 ----- 21

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Qy  21 ----- 21

Db 19625 AAAACATTACTAAAAAANAACCTATACCGAAAAACGTAACAAAAAATTCATATC 19566

Qy  22 -----Pro 22
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Db 19565 TCCGAAAAAATCAACCCCTAACTACTAAATCCCTAAACTATATCTTCTAAATCCGCAAAACCG 19506

Qy  23  GlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyrGluSer 42
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Qy  43  SerPheLeuGluLeuLeuGluLys----- 50
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QY 50 ----- 50

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QY 59 SerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 19265 TCAAAACCAACGTCACCTCCACCACATAACAAATCTCAACACCATATTAATACACACA 19206

RESULT 15
RN510D20
LOCUS
DEFINITION Rattus norvegicus clone RPCI-31-510D20 strain Brown Norway, ***
SEQUENCING IN PROGRESS ***, 116 unordered pieces.
ACCESSION AL603723
VERSION AL603723.2 GI:17154525
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 Sudbrak, R., Borzym, K., Mueller, I., Klages, S., Kosiura, A., and
Walter, L., Guenther, E., Hurt, P., Lehrach, H., Himmelbauer, H. and
Reinhardt, R.
Unpublished
2 (bases 1 to 132977)
Direct Submission
Submitted (10-AUG-2001) MPIMG, Abt. Lehrach, Max Planck Institut
Fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany
On Nov 29, 2001 this sequence version replaced gi:15149843.
COMMENT
contig 01 1. 1705
contig 02 1806. .2557
contig 03 2658. .2942
contig 04 3043. .3428
contig 05 3529. .4577
contig 06 4678. .5343
contig 07 5444. .6200
contig 08 6301. .6738
contig 09 6839. .7212
contig 10 7313. .7774
contig 11 7875. .8129
contig 12 8230. .9449
contig 13 9350. .10193
contig 14 10294. .11201
contig 15 11302. .11633
contig 16 11734. .12087
contig 17 12188. .12362
contig 18 12463. .12523
contig 19 12624. .12739
contig 20 12900. .13207
contig 21 13308. .13597
contig 22 13698. .13935
contig 23 14036. .14242
contig 24 14343. .14667
contig 25 14768. .15008
contig 26 15109. .15353
contig 27 15454. .15610
contig 28 15711. .16120
contig 29 16221. .16339
contig 30 16440. .16712
contig 31 16813. .17073
contig 32 17174. .17380
contig 33 17481. .17661
contig 34 17762. .18261

contig 35 18362. .18967
contig 36 19068. .22083
contig 37 22184. .23276
contig 38 23377. .25592
contig 39 25693. .26310
contig 40 26411. .27258
contig 41 27359. .31077
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contig 46 37769. .38782
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contig 65 60414. .61579
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contig 69 66374. .68109
contig 70 68210. .69847
contig 71 69948. .71958
contig 72 72059. .74880
contig 73 74781. .78049
contig 74 78150. .80892
contig 75 80993. .81370
contig 76 81471. .84472
contig 77 84573. .85382
contig 78 85483. .89384
contig 79 89485. .91007
contig 80 91108. .92068
contig 81 92169. .96829
contig 82 96930. .97851
contig 83 98052. .99891
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contig 91 111112. .111870
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contig 100 121499. .122192
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contig 105 124013. .124565
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contig 108 125786. .125935
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contig 111 127184. .127851
contig 112 127952. .128311
contig 113 128412. .130249
contig 114 130350. .131023
contig 115 131124. .132137
contig 116 132238. .132977.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 116 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1705: contig of 1705 bp in length
* 1706 1805: gap of 100 bp
* 1806 2557: contig of 752 bp in length
* 2558 2657: gap of 100 bp
* 2658 2942: contig of 285 bp in length
* 2943 3042: gap of 100 bp
* 3043 3428: contig of 386 bp in length
* 3429 3528: gap of 100 bp
* 3529 4577: contig of 1049 bp in length
* 4578 4677: gap of 100 bp
* 4678 5343: contig of 666 bp in length
* 5344 5443: gap of 100 bp
* 5444 6200: contig of 757 bp in length
* 6201 6300: gap of 100 bp
* 6301 6738: contig of 438 bp in length
* 6739 6838: gap of 100 bp
* 6839 7212: contig of 374 bp in length
* 7213 7312: gap of 100 bp
* 7313 7774: contig of 462 bp in length
* 7775 7874: gap of 100 bp
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* 8130 8229: gap of 100 bp
* 8230 9449: contig of 1220 bp in length
* 9450 9549: gap of 100 bp
* 9550 10193: contig of 644 bp in length
* 10194 10293: gap of 100 bp
* 10294 11201: contig of 908 bp in length
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* 11634 11733: gap of 100 bp
* 11734 12087: contig of 354 bp in length
* 12088 12187: gap of 100 bp
* 12188 12362: contig of 175 bp in length
* 12363 12462: gap of 100 bp
* 12463 12523: contig of 61 bp in length
* 12524 12623: gap of 100 bp
* 12624 12799: contig of 176 bp in length
* 12800 12899: gap of 100 bp
* 12900 13207: contig of 308 bp in length
* 13208 13307: gap of 100 bp
* 13308 13597: contig of 290 bp in length
* 13598 13697: gap of 100 bp
* 13698 13935: contig of 238 bp in length
* 13936 14035: gap of 100 bp
* 14036 14242: contig of 207 bp in length
* 14243 14342: gap of 100 bp
* 14343 14667: contig of 325 bp in length
* 14668 14767: gap of 100 bp
* 14768 15008: contig of 241 bp in length
* 15009 15108: gap of 100 bp
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Alignment Scores:

Pred. No.:	0.0018	Length:	132977
Score:	121.00	Matches:	30
Percent Similarity:	36.94%	Conservative:	11
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Query Match:	30.33%	Indels:	56
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US-09-092-296-15 (1-78) x RN510D20 (1-132977)

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Qy	39	SerTyrGluSerPheLeuGluLeuLys-----	50
Db	8806	TCCCAAGACTCCGGCTTCTGGACATGCTCCAAAAGTAGTTTTTAGGAAGCAGGATGGG	8865
Qy	50	-----	50
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Qy	50	-----	50
Db	8926	GGGGGTGGCTGAGTTAAGCAGGGAGTGGGGTTACCATCTTAGACCTCATCCTCCATTCAT	8985
Qy	51	-----LeuCysLeuLeuLeuHisLeuProSerGlyThrSerValThrLeu	65
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Qy	66	HisHisAlaArgSerGlnHisHisValValCys	76
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Search completed: May 1, 2003, 05:43:06
Job time : 1315 secs


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; STRANDEDNESS: single
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US-09-092-296-6

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RESULT 2
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; Sequence 362, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1997-11-24
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; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGGTCTGGGCTGGCCCTTGTCTCTCTTGCACCTCTTGGCAGCTCACATGGAACA 60
Db 58 ATGGGGTCTGGGCTGGCCCTTGTCTCTCTTGCACCTCTTGGCAGCTCACATGGAACA 117
QY 61 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 120
Db 118 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 177
QY 121 GAGTCCAGCTTCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGG 180
Db 178 GAGTCCAGCTTCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGG 237
QY 181 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 238 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 3

US-09-989-293A-362
; Sequence 362, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186

1	;	PRIOR FILING DATE:	1997-11-12	
2	;	PRIOR APPLICATION NUMBER:	60/065311	
3	;	PRIOR FILING DATE:	1997-11-13	
4	;	PRIOR APPLICATION NUMBER:	60/066770	
5	;	PRIOR FILING DATE:	1997-11-24	
6	;	PRIOR APPLICATION NUMBER:	60/075945	
7	;	PRIOR FILING DATE:	1998-02-25	
8	;	PRIOR APPLICATION NUMBER:	60/078910	
9	;	PRIOR FILING DATE:	1998-03-20	
10	;	PRIOR APPLICATION NUMBER:	60/083322	
11	;	PRIOR FILING DATE:	1998-04-28	
12	;	PRIOR APPLICATION NUMBER:	60/084600	
13	;	PRIOR FILING DATE:	1998-05-07	
14	;	PRIOR APPLICATION NUMBER:	60/087106	
15	;	PRIOR FILING DATE:	1998-05-28	
16	;	PRIOR APPLICATION NUMBER:	60/087607	
17	;	PRIOR FILING DATE:	1998-06-02	
18	;	PRIOR APPLICATION NUMBER:	60/087609	
19	;	PRIOR FILING DATE:	1998-06-02	
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21	;	PRIOR FILING DATE:	1998-06-02	
22	;	PRIOR APPLICATION NUMBER:	60/087827	
23	;	PRIOR FILING DATE:	1998-06-03	
24	;	PRIOR APPLICATION NUMBER:	60/088021	
25	;	PRIOR FILING DATE:	1998-06-04	
26	;	PRIOR APPLICATION NUMBER:	60/088025	
27	;	PRIOR FILING DATE:	1998-06-04	
28	;	PRIOR APPLICATION NUMBER:	60/088026	
29	;	PRIOR FILING DATE:	1998-06-04	
30	;	PRIOR APPLICATION NUMBER:	60/088028	
31	;	PRIOR FILING DATE:	1998-06-04	
32	;	PRIOR APPLICATION NUMBER:	60/088029	
33	;	PRIOR FILING DATE:	1998-06-04	
34	;	PRIOR APPLICATION NUMBER:	60/088030	
35	;	PRIOR FILING DATE:	1998-06-04	
36	;	PRIOR APPLICATION NUMBER:	60/088033	
37	;	PRIOR FILING DATE:	1998-06-04	
38	;	PRIOR APPLICATION NUMBER:	60/088326	
39	;	PRIOR FILING DATE:	1998-06-04	
40	;	PRIOR APPLICATION NUMBER:	60/088167	
41	;	PRIOR FILING DATE:	1998-06-05	
42	;	PRIOR APPLICATION NUMBER:	60/088202	
43	;	PRIOR FILING DATE:	1998-06-05	
44	;	PRIOR APPLICATION NUMBER:	60/088212	
45	;	PRIOR FILING DATE:	1998-06-05	
46	;	PRIOR APPLICATION NUMBER:	60/088217	
47	;	PRIOR FILING DATE:	1998-06-05	
48	;	PRIOR APPLICATION NUMBER:	60/088655	
49	;	PRIOR FILING DATE:	1998-06-09	
50	;	PRIOR APPLICATION NUMBER:	60/088734	
51	;	PRIOR FILING DATE:	1998-06-10	
52	;	PRIOR APPLICATION NUMBER:	60/088738	
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55	;	PRIOR FILING DATE:	1998-06-10	
56	;	PRIOR APPLICATION NUMBER:	60/088810	
57	;	PRIOR FILING DATE:	1998-06-10	
58	;	PRIOR APPLICATION NUMBER:	60/088824	
59	;	PRIOR FILING DATE:	1998-06-10	
60	;	PRIOR APPLICATION NUMBER:	60/088826	
61	;	PRIOR FILING DATE:	1998-06-10	
62	;	PRIOR APPLICATION NUMBER:	60/088858	
63	;	PRIOR FILING DATE:	1998-06-11	
64	;	PRIOR APPLICATION NUMBER:	60/088861	
65	;	PRIOR FILING DATE:	1998-06-11	
66	;	PRIOR APPLICATION NUMBER:	60/088876	
67	;	PRIOR FILING DATE:	1998-06-11	
68	;	PRIOR APPLICATION NUMBER:	60/089105	
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70	;	PRIOR APPLICATION NUMBER:	60/089440	
71	;	PRIOR FILING DATE:	1998-06-16	
72	;	PRIOR APPLICATION NUMBER:	60/089512	
73	;	PRIOR FILING DATE:	1998-06-16	

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: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091478
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091544
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091519
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091626
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091633
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091978
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/091982
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/092182
: PRIOR FILING DATE: 1998-07-09

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Query Match      100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels
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QY	1	ATGGGGTCTGGGGTGCCTCTGTCCTCTTTGACCTCCTTGGCAGCTC	60
		ACATGGGAACA	
DB	58	ATGGGGTCTGGGGTGCCTCTTGTACCTCCTTGGCAGCTC	117
		ACATGGGAACA	
QY	61	GGGCGCGGATGACATTTGCACACTGAAGCTGAAGGAGCTTTTCTG	120
		ACAAATTCCTCCTAT	
DB	118	GGGCGCGGATGACATTTGCACACTGAAGCTGAAGGAGCTTTTCTG	177
		ACAAATTCCTCCTAT	
QY	121	GAGTCCAGCTTCTCGAATGCTGTAAGAGCTCTGCTCTCTCCATC	180
		CTCCCTTCAGG	
DB	178	GAGTCCAGCTTCTCGAATGCTGTAAGAGCTCTGCTCTCCATC	237
		CTCCCTTCAGG	
QY	181	ACGAGCTCACCTCCACATGCAAGATCTCAACACCATGTTCTGTG	234
		CAACA	
DB	238	ACGAGCTCACCTCCACATGCAAGATCTCAACACCATGTTCTGTG	291
		CAACA	

RESULT 4

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US-10-063-547-65
; Sequence 65, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOT
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-063-547-65

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Qy 1 ATGGGCTCTGGGCTGCCCTTGTCTCCTCTTGACCCCTCCTTGGCAGCTCACATGAACA 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 ATGGGGTCWGGGCGCCCCCTGTCTCCTTGACCCTCCTTGGCAGCTCACATGAACA 117

Qy	61	GGGCGGGGATGAC	TTGCAACTGAGCTGAGGAGTCTTTCTGCAAAATTCCTCTAT	120
Db	118	GGGCGGGGATGAC	TTTCTGCAAAATTCCTCTAT	177
Qy	121	GAGTCCAGCTTC	TGTAATGCTGTGAAAGCTCGCTCCCTCCATCCCTTCAGGG	180
Db	178	GAGTCCAGCTTC	TGTAATGCTGTGAAAGCTCGCTCCCTCCATCCCTTCAGGG	237
Qy	181	ACGACGGTACCC	TCCACCATCGAAGATCTCAACACCACCATGTTGTCTGCAACACA	234
Db	238	ACGACGGTACCC	TCCACCATCGAAGATCTCAACACCACCATGTTGTCTGCAACACA	291

RESULT, T 5

US-09-989-735-362
; Sequence 362, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PLC61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759

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; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
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; PRIOR APPLICATION NUMBER: 60/089948
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; PRIOR FILING DATE: 1998-06-19
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; PRIOR APPLICATION NUMBER: 60/090444
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTGGGCTGCCCTTGTCTCTCTTGTGACCCCTCTTGGCAGCTCACATGGAACA 60
DB 58 ATGGGCTGGGCTGCCCTTGTCTCTCTTGTGACCCCTCTTGGCAGCTCACATGGAACA 117
QY 61 GGCCCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTGTGACAAATTCCTCCTAT 120
DB 118 GGCCCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTGTGACAAATTCCTCCTAT 177
QY 121 GAGTCAGCTTCTCTGGAATTGCTTGAAGCTGCGCTCTCTCTCTCTCTCTCTCTCAGG 180
DB 178 GAGTCAGCTTCTCTGGAATTGCTTGAAGCTGCGCTCTCTCTCTCTCTCTCTCTCAGG 237
QY 181 ACCAGGCTCACCTCCACCATGCAAGATCTCAACCATGTTCTCTGCAACACA 234
DB 238 ACCAGGCTCACCTCCACCATGCAAGATCTCAACCATGTTCTCTGCAACACA 291

RESULT 7
US-09-989-730-362
; Sequence 362, Application US/09989730
; Publication No. US2002019767A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C69
; CURRENT APPLICATION NUMBER: US/09/989,730
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322

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2 PRIOR APPLICATION NUMBER: 60/084600
3 PRIOR FILING DATE: 1998-05-07
4 PRIOR APPLICATION NUMBER: 60/087106
5 PRIOR FILING DATE: 1998-05-28
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8 PRIOR APPLICATION NUMBER: 60/087609
9 PRIOR FILING DATE: 1998-06-02
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12 PRIOR APPLICATION NUMBER: 60/087827
13 PRIOR FILING DATE: 1998-06-03
14 PRIOR APPLICATION NUMBER: 60/088021
15 PRIOR FILING DATE: 1998-06-04
16 PRIOR APPLICATION NUMBER: 60/088025
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26 PRIOR APPLICATION NUMBER: 60/088033
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83 PRIOR FILING DATE: 1998-06-18
84 PRIOR APPLICATION NUMBER: 60/089947
85 PRIOR FILING DATE: 1998-06-19
86 PRIOR APPLICATION NUMBER: 60/089948
87 PRIOR FILING DATE: 1998-06-19
88 PRIOR APPLICATION NUMBER: 60/089952
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130 PRIOR APPLICATION NUMBER: 60/090696
131 PRIOR FILING DATE: 1998-06-25
132 PRIOR APPLICATION NUMBER: 60/090862
133 PRIOR FILING DATE: 1998-06-26
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137 PRIOR FILING DATE: 1998-06-26
138 PRIOR APPLICATION NUMBER: 60/091478
139 PRIOR FILING DATE: 1998-07-01
140 PRIOR APPLICATION NUMBER: 60/091478
141 PRIOR FILING DATE: 1998-07-02
142 PRIOR APPLICATION NUMBER: 60/091544
143 PRIOR FILING DATE: 1998-07-01
144 PRIOR APPLICATION NUMBER: 60/091519
145 PRIOR FILING DATE: 1998-07-02
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148 PRIOR APPLICATION NUMBER: 60/091633
149 PRIOR FILING DATE: 1998-07-02

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTGTGGGCTGCCCTTGTCTCTTGACCCCTCTTGCGAGCTCATCATGGAACA 60
    |||||
Db 58 ATGGGCTGTGGGCTGCCCTTGTCTCTCTTGACCCCTCTTGCGAGCTCATCATGGAACA 117
    |||||

QY 61 GGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 120
    |||||
Db 118 GGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177
    |||||

QY 121 GAGTCAGCTTCCTGGAAATGCTTTGAAAAGCTTGCCTCTCTCGATCTCCCTTCAGGG 180
    |||||
Db 178 GAGTCAGCTTCCTGGAAATGCTTTGAAAAGCTTGCCTCTCTCGATCTCCCTTCAGGG 237
    |||||

QY 181 ACCAGGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
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Db 238 ACCAGGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291
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RESULT 8
US-09-990-436-362
; Sequence 362, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C14
; CURRENT APPLICATION NUMBER: US/09/990,436
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 234; DB 9; Length 422;

Best Local Similarity 100.0%; Pred. No. 2.6e-71;

Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGTCTGGGCTGCCCTTGCTCTCTTGACCTCTTGAGCGCTCACATGGGAACA 60

DB 58 ATGGGGTCTGGGCTGCCCTTGCTCTCTTGACCTCTTGAGCGCTCACATGGGAACA 117

QY 61 GGCCCGGATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 120

DB 118 GGCCCGGATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 177

QY 121 GAGTCACGCTTCCTGGAATGCTTGAAAGCTCTGCTCCTCCTCCATCCTCCTCAGG 180

DB 178 GAGTCACGCTTCCTGGAATGCTTGAAAGCTCTGCTCCTCCTCCATCCTCCTCAGG 237

QY 181 ACAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234

DB 238 ACAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 9

US-09-991-181-362

; Sequence 362, Application US/09991181

; Publication No. US20020197615A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C53

; CURRENT APPLICATION NUMBER: US/09/991,181

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

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; PRIOR FILING DATE: 1997-10-17

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;; PRIOR FILING DATE: 1998-06-12
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;; PRIOR FILING DATE: 1998-06-16
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTCTGGGCTGCCCTTGTCTCTCTTGTGACCTCTTGGCAGCTCAGCTGGAACA 60
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Db 58 ATGGGCTCTGGGCTGCCCTTGTCTCTCTTGTGACCTCTTGGCAGCTCAGCTGGAACA 117
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QY 61 GGCGCGGGTATGACTTTCACACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 120
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Db 118 GGCGCGGGTATGACTTTCACACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177
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QY 121 GAGTCAGCTTCTCTGGAATTCCTGAAAGCTCTGAAAAGCTCTGCTCTCTCTCCATCCCTTCAGG 180
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Db 178 GAGTCAGCTTCTCTGGAATTCCTGAAAGCTCTGAAAAGCTCTGCTCTCTCCATCCCTTCAGG 237
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QY 181 ACCAGGCTCAGCCCTCCAGCATGCAAGATCTCAACACCATGTTCTGTCGAACA 234
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Db 238 ACCAGGCTCAGCCCTCCAGCATGCAAGATCTCAACACCATGTTCTGTCGAACA 291
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RESULT 11
US-09-989-734-362
; Sequence 362, Application US/09989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; CURRENT APPLICATION NUMBER: US/09/989,734
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0% Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 58 ATGGGGTCTGGGCTGCCCTTGTCTCTTGTGACCCCTCTTGGCAGCTCACATGAACA 117
Qy 61 GGGCGGGTATGACTTTGCAACTGAAGTGAAGAGTCTTTCTGACAAAATTCCTCTAT 120
Db 118 GGGCGGGTATGACTTTGCAACTGAAGTGAAGAGTCTTTCTGACAAAATTCCTCTAT 177
Qy 121 GAGTCCAGCTTCTCTGGAATTCCTTGAAGAGTCTGCTCTCTCTCCATCTCCCTCAGGG 180
Db 178 GAGTCCAGCTTCTCTGGAATTCCTTGAAGAGTCTGCTCTCTCTCCATCTCCCTCAGGG 237
Qy 181 ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 238 ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 13
US-10-174-590-241
; Sequence 241, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Zhang, William I.
; APPLICANT: Zhong, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C42

; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-241

Query Match 100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 121 GAGTCCAGCTTCCCTGGAATTCCTGAAAGCTGCGCTCTCTCCATCTCCCTCAGG 180
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178 GAGTCCAGCTTCCCTGGAATTCCTGAAAGCTGCGCTCTCTCCATCTCCCTCAGG 237
QY 181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTTCTGCAACACA 234
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
238 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTTCTGCAACACA 291

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; Sequence 241, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
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; ORGANISM: Homo Sapien
US-10-176-758-241

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DB 178 GAGTCCAGCTTCCCTGGAATTCCTGAAAGCTGCGCTCTCTCCATCTCCCTCAGG 237
QY 181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTTCTGCAACACA 234
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 15
US-10-063-616-65
; Sequence 65, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-65

Query Match 100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
58 ATGGGCTCGGGCTGCCCTTGCCTCTTGCACCTCTCTGGAGCTGCATGGAACA 117
QY 61 GGGCCGGGTATGACTTTGCAACTGAAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTAT 120
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 121 GAGTCCAGCTTCCCTGGAATTCCTGAAAGCTGCGCTCTCTCCATCTCCCTCAGG 180
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTTCTGCAACACA 234
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
238 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTTCTGCAACACA 291

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Job time : 64.8775 secs

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 Copyright (c) 1993 - 2003 CompuGen Ltd.
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 Gapop 10.0 , Gapext 1.0
 Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	30.8	13.2	7218	1 US-08-232-463-14	Sequence 14, Appl
c 3	30.6	13.1	1956	4 US-09-484-970B-38	Sequence 38, Appl
c 4	30	12.8	176373	3 US-09-128-155-17	Sequence 17, Appl
c 5	29.8	12.7	1091	4 US-09-219-194-2	Sequence 2, Appl
c 6	29	12.4	3580	4 US-09-081-345-1	Sequence 1, Appl
c 7	28.6	12.2	2662	3 US-08-750-357-8	Sequence 8, Appl
c 8	28.4	12.1	3218	4 US-09-369-364A-6	Sequence 6, Appl
c 9	28.4	12.1	7812	4 US-09-368-590-1	Sequence 4, Appl
c 10	28.2	12.1	2718	4 US-09-360-186-4	Sequence 1, Appl
c 11	28.2	12.1	3099	4 US-09-360-186-2	Sequence 2, Appl
c 12	28.2	12.1	31431	4 US-09-360-186-1	Sequence 1, Appl
c 13	28	12.0	5962	1 US-08-188-582-10	Sequence 10, Appl
c 14	28	12.0	5962	1 US-08-646-715-10	Sequence 10, Appl
c 15	27.8	11.9	2782	2 US-09-937-466-1	Sequence 1, Appl
c 16	27.8	11.9	2782	2 US-09-172-528-1	Sequence 1, Appl
c 17	27.8	11.9	2782	3 US-09-318-199-1	Sequence 1, Appl
c 18	27.8	11.9	2782	4 US-09-503-579-1	Sequence 1, Appl
c 19	27.8	11.9	2870	4 US-09-221-017B-850	Sequence 850, Appl
c 20	27.6	11.8	1293	4 US-09-381-681-1	Sequence 1, Appl
c 21	27.6	11.8	1360	4 US-09-191-136-30	Sequence 30, Appl
c 22	27.6	11.8	1697	4 US-09-381-681-2	Sequence 2, Appl
c 23	27.6	11.8	1853	1 US-08-553-110-2	Sequence 2, Appl
c 24	27.6	11.8	2635	4 US-09-186-276B-57	Sequence 57, Appl
c 25	27.6	11.8	2635	4 US-08-842-445-57	Sequence 57, Appl
c 26	27.6	11.8	2635	4 US-09-186-188B-57	Sequence 57, Appl
c 27	27.6	11.8	4279	4 US-09-041-886-22	Sequence 22, Appl

c 28	27.4	11.7	984	4 US-08-927-219-52	Sequence 52, Appl
c 29	27.4	11.7	10014	4 US-08-927-219-130	Sequence 130, Appl
c 30	27.4	11.7	10482	4 US-09-322-478-23	Sequence 23, Appl
c 31	27.2	11.6	1295	4 US-09-219-194-3	Sequence 3, Appl
c 32	27.2	11.6	2121	1 US-08-331-394-3	Sequence 3, Appl
c 33	27.2	11.6	2121	1 US-08-250-858-3	Sequence 3, Appl
c 34	27.2	11.6	2121	1 US-08-446-915-3	Sequence 3, Appl
c 35	27.2	11.6	2121	2 US-08-744-139-3	Sequence 3, Appl
c 36	27.2	11.6	2121	5 PCT-US95-06639-3	Sequence 3, Appl
c 37	27.2	11.6	2532	4 US-09-361-631-4	Sequence 4, Appl
c 38	27	11.5	1785	3 US-08-729-416C-8	Sequence 8, Appl
c 39	27	11.5	1980	2 US-08-766-858A-4	Sequence 4, Appl
c 40	27	11.5	2459	1 US-08-101-593-5	Sequence 5, Appl
c 41	27	11.5	2459	1 US-08-465-995A-5	Sequence 5, Appl
c 42	27	11.5	2459	2 US-08-465-994C-5	Sequence 5, Appl
c 43	26.8	11.5	2259	6 5185254-3	Patent No. 5185254
c 44	26.8	11.5	16063	4 US-09-801-052-3	Sequence 3, Appl
c 45	26.6	11.4	999	1 US-08-416-478A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
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 ; Sequence 798, Application US/09221017B
 ; Patent No. 6444799
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSS, Bruce C.
 ; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 1120
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 PAGE MILL ROAD
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/221.017B
 ; FILING DATE: 23-DEC-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PP1182
 ; FILING DATE: 31-DEC-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PP1546
 ; FILING DATE: 30-JAN-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PP2911
 ; FILING DATE: 09-APR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/AU98/01023
 ; FILING DATE: 10-DEC-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Morroy, Gladys H
 ; REGISTRATION NUMBER: 32,430
 ; REFERENCE/DOCKET NUMBER: 27340-20021.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-813-5600
 ; TELEFAX: 650-494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 798:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1537 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular

Best Local Similarity 3.5%; Pred. No. 2.1;
Matches 8; Conservative 128; Mismatches 90; Indels 0; Gaps 0;

[illegible]

```

RESULT 3
US-09-484-970B-38/c
> Sequence 38, Application US/09484970B
> Patent No. 6426186
> GENERAL INFORMATION:
> APPLICANT: Jones, Karen A.
> APPLICANT: Volkmut, Wayne
> APPLICANT: Walker, Michael G.
> TITLE OF INVENTION: BONE REMODELING GENES
> FILE REFERENCE: PB-0014 US
> CURRENT APPLICATION NUMBER: US/09/484,970B
> CURRENT FILING DATE: 2000-01-18
> NUMBER OF SEQ ID NOS: 172
> SOFTWARE: PERL Program
> SEQ ID NO 38
> LENGTH: 1956
> TYPE: DNA
> ORGANISM: Homo sapiens
> FEATURE:
> NAME/KEY: misc_feature
> OTHER INFORMATION: Incyte ID NO. 6426186 247608.1CB1
US-09-484-970B-38

```

	Query Match	13.18;	Score 30.6;	DB 4;	Length 1956;
	Best Local Similarity	50.3%;	Pred. No. 1.4;		
	Matches 75;	Conservative	0;	Mismatches 74;	Indels 0; Gaps
Qy	72	GACTTTGCACTCAAGCTGAAGGAGTCTTTTCTGCACAAATTCCTCTATGAGTCCAGCITT	131		
Dd	399	GATTTTCTTCCTTAACTGGCATCTACTCTTGACAGAGATCTTCAAGTGTGTGTTGGAGT	340		
Qy	132	CCTGGAATTGCTTGAAGAAGCTCTGCCCTCTCCATCCCTTCAGGACACCGACGTCAC	191		
Dd	339	CCAACACTTGNATTAATAAGTCTTTTTTTCTCCAGTCCACTTTCATTTCAGCATCAA	280		
Qy	192	CCTCCACCATGCAAGATCFCAACCAATG	220		
Dd	279	CTGCATTCATGTCAGCATTCATCATCTTG	251		

APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE OF INVENTION: 094/04/052001
FILE REFERENCE: 094/04/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02

;
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match 12.8%; Score 30; DB 3; Length 176373;
Best Local Similarity 55.9%; Pred. No. 16;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 73 ACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTC 132
Db 137160 ACTCTACAGCTGGAGTAAGTGAATGCTATGGAATGAAGCCCTCTCAGCCCTCTGCTAC 137101

QY 133 CTGGAATGCTTGAAGCTCTGCCTCCCTCCCTCCATCCCT 174
Db 137100 CACTTATCCAGACACCACTCTCTCCCGGCCCATCCCT 137059

RESULT 5
US-09-219-194-2
; Sequence 2, Application US/09219194
; Patent No. 6410230
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; TITLE OF INVENTION: GLYCERALDEHYDE-3-PHOSPHATE
; DEHYDROGENASE AND NUCLEAR RESTORATION OF CYTOPLASMIC MALE
; STERILITY

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SWABY OGILVY RENAULT
STREET: 1981 McGill College Ave. - Suite 1600
CITY: Montreal
STATE: QC
COUNTRY: Canada
ZIP: H3A 2Y3

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/219,194
FILING DATE: 23-Dec-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/020,553
FILING DATE: 26-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cote, France

REGISTRATION NUMBER: 4166
REFERENCE/DOCKET NUMBER: 1770-152*PCT* FC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 514 845-7126
TELEFAX: 514-288-8389
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-219-194-2

Query Match 12.7%; Score 29,8; DB 4; Length 1091;
Best Local Similarity 51.9%; Pred. No. 2;
Matches 67; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 39 CCITGGCAGCTCACATGGAACAGGCGGGGTATGACTTTGCAACTGAAGCTGAAGAGTC 98
Db 263 CCTGAGGATATCCCATGGGTGGAGCGGAGCTGACTTTGTTGAGTCTACTGGTGC 322

QY 99 TTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCTCGAATTTGTTGAAAAGCTCTCGCT 158
Db 323 TTCACCTGACAAGGACAAGGCTGCTCACTTGAGGGTGTGCCAAGAAAGTTGTCTATC 382

QY 159 CCTCCTCCA 167
Db 383 TCTGCACCA 391

RESULT 6
US-09-081-345-1/c
; Sequence 1, Application US/09081345
; Patent No. 6228641
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; APPLICANT: Gregory D. Plowman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,345
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,222
FILING DATE: May 20, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/253
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3580 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-081-345-1

Query Match 12.4%; Score 29; DB 4; Length 3580;
Best Local Similarity 48.0%; Pred. No. 6.1;
Matches 83; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 23 TCCTCCTCTTGACCCCTCCCTGCGAGCTCACATGGAACAGGCGCGGTATGACTTTGCAAC 82
Db 642 TCATGGTCTGGCCAATTCCTGTAATGAAACTGCTAGATAGTTCCAGATTTCACATTGAC 583

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QY 83 TGAAGCTGAAGAGTCTTTCTTGACAAATTCCTCTATGAGTCCAGCTTCTCGAATTGC 142
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 582 TTAACCTTTAGAGCTCGATTATATATACAGATTCTCTTTTTCAGCTTCACAGGATACA 523
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 143 TTGAAAGCTGTGCTCTCTCTCCATCTCCCTTCAGGACCGAGCGTCACCCCTC 195
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 522 GAGAAAGGCCAAATTCACGTCGATCTCTCTGGCTCAGCCAGTAGGCGTC 470
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-08-750-357-8/c
; Sequence 8, Application US/08750357
; Patent No. 6008437
; GENERAL INFORMATION:
; APPLICANT: KREBBERS, Enno
; APPLICANT: WILLIAMS, Mark
; APPLICANT: LEEMANS, Jan
; TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
; TITLE OF INVENTION: MALE STERILE PLANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,357
; FILING DATE: 21-WAR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 018030-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-750-357-8

Query Match 12.2%; Score 28.6; DB 3; Length 2662;
Best Local Similarity 61.3%; Pred. No. 7.2;
Matches 46; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 157 CTCCTCTCCATCTCCCTTCAGGACGAGCGTCACCCCTCCACCATGCAAGATCTCAACAC 216
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1212 CTCCTCTCCACCGGTTTCAGGTCGCGCGCGGACACCAAGAGCCCTCCACA 1153
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 217 CATGTTGTCTGCAAC 231
|||||
Db 1152 AAAACGGACGCAAC 1138
|||||

RESULT 8
US-09-369-364A-6/c
; Sequence 6, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
```

```
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3218
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(3003)
US-09-369-364A-6

Query Match 12.1%; Score 28.4; DB 4; Length 3218;
Best Local Similarity 48.7%; Pred. No. 9.1;
Matches 77; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 4 GGGTCGGGCTGCCCTTGTCTCTTGGACCTCTTGGCAGCTCACATGGAACAGGG 63
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2838 GGGCTGTGGCTGCCCTCTCTACCTCTGCGCAGTGACTGTGCACCTTGGTCCAGGG 2779
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 64 CCGGATATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAG 123
|| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2778 CCCATAATCCAGGAGAACACACGGGGCGGGACCTCTGTCGGCCACCTGCTCCCTGTG 2719
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 124 TCCAGCTTCTCGAATTGCTTGAAGAAGCTCTGCTCTCT 161
|| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2718 GATGGTGACTCGTAGTGCACCCAGGGTTGCTCTCT 2681
|| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-09-368-590-1/c
; Sequence 1, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
; FILE REFERENCE: 101918-200 (OCR-941)
; CURRENT APPLICATION NUMBER: US/09/368,590
; CURRENT FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7812
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6879)
; NAME/KEY: unsure
; LOCATION: (100)...(102)
; NAME/KEY: unsure
; LOCATION: (1021)...(1023)
; NAME/KEY: unsure
; LOCATION: (2266)...(2268)
US-09-368-590-1

Query Match 12.1%; Score 28.4; DB 4; Length 7812;
Best Local Similarity 62.9%; Pred. No. 13;
Matches 44; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 159 COTCTCCATCTCCCTTCAGGACGAGCTCACCCCTCCACCATGCAAGATCTCAACACCA 218
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 886 COTTCACCCCTCGCTCTGGGCGCATGTCCTCCAGCAGTCCATGCTTCTTCTGCAACA 827
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 219 TGTGTCTGC 228
|| ||| |||
Db 826 GGTGCTCTGC 817
|| ||| |||
```

RESULT 10
US-09-360-186-4/c
; Sequence 4, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: Bs2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; EARLIER FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2718
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2718)
US-09-360-186-4

Query Match 12.1%; Score 28.2; DB 4; Length 2718;
Best Local Similarity 50.4%; Pred. No. 9.9;
Matches 69; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 96 GTCTTTTCTGACAAATTCCTCTATGAGTCAGCTTCTGGAATTCCTGAAATTCCTGAAAGCTCTG 155
DB 1390 GACTTCTCTGTGTGACGAGGACTAGACATCTATCGACAAGCTCTTCAAACACTTCTCAA 1331
QY 156 GTCTTTTCTGACAAATTCCTCTATGAGTCAGCTTCTGGAATTCCTGAAATTCCTGAAAGCTCTG 155
DB 1330 GACTTCTCTGTGTGACGAGGACTAGACATCTATCGACAAGCTCTTCAAACACTTCTCAA 215
QY 216 CCATGTTGTCGCAACA 232
DB 1270 AATTCCTCACTGGAATA 1254

RESULT 11
US-09-360-186-2/c
; Sequence 2, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: Bs2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; EARLIER FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)..(2810)
US-09-360-186-2

Query Match 12.1%; Score 28.2; DB 4; Length 3099;
Best Local Similarity 50.4%; Pred. No. 10;
Matches 69; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 96 GTCTTTTCTGACAAATTCCTCTATGAGTCAGCTTCTGGAATTCCTGGAATTCCTGAAAGCTCTG 155
DB 1482 GACTTCTCTGTGACGAGGACTAGACATCTATCGACAAGCTCTTCAAACACTTCTCAA 1423

QY 156 CCTCTCTCTCCATCTCCTTCAGGGACCAGCGTCACCCCTCCACCATGCAAGATCTCAACA 215
DB 1422 CCTCTCTCTCCAAATCATTTTCCAACTTCAGGAACCCCTCAGCCATCCATGATCTCATCA 1363
QY 216 CCATGTTGTCGCAACA 232
DB 1362 AATTCCTCACTGGAATA 1346

RESULT 12
US-09-360-186-1/c
; Sequence 1, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: Bs2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; EARLIER FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 31491
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-360-186-1

Query Match 12.1%; Score 28.2; DB 4; Length 31491;
Best Local Similarity 50.4%; Pred. No. 29;
Matches 69; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 96 GTCTTTTCTGACAAATTCCTCTATGAGTCAGCTTCTGGAATTCCTGAAATTCCTGAAAGCTCTG 155
DB 2869 GACTTCTCTGTGTGACGAGGACTAGACATCTATCGACAAGCTCTTCAAACACTTCTCAA 2810
QY 156 CCTCTCTCTCCATCTCCTTCAGGACCAGGTCACCCCTCCACCATGCAAGATCTCAACA 215
DB 2809 CCTCTCTCTCCAAATCATTTTCCAACTTCAGGAACCCCTCAGCCATCCATGATCTCATCA 2750
QY 216 CCATGTTGTCGCAACA 232
DB 2749 AATTCCTCACTGGAATA 2733

RESULT 13
US-08-188-582-10/c
; Sequence 10, Application US/08188582
; Patent No. 5534410
; GENERAL INFORMATION:
; APPLICANT: Tjian, Robert
; APPLICANT: Comai, Lucio
; APPLICANT: Dynlacht, Brian D.
; APPLICANT: Hoey, Timothy
; APPLICANT: Ruppert, Siegfried
; APPLICANT: Tanese, Naoko
; APPLICANT: Wang, Edith
; APPLICANT: Weinzierl, Robert O.J.
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ELEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5962 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 14..5692
US-08-188-582-10

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Query Match	12.0%	Score 28	DB 1	Length 5962	
Best Local Similarity	48.2%	Pred. No. 16			
Matches 79	Conservative	0	Mismatches 85	Indels 0	Gaps 0
QY	11	GGCTGGCCCTTGTCTCTCTTGGACCCCTCTTGGCAGCTCACAATGGAACAGGCGCGGTA	70		
Db	3993	GTCTTTTCCAACCTCTCTCTGTCTTCTGTGTCATGGCAACAGGTTGGAAGTGGCGCA	3934		
QY	71	TGACTTTGGCACTGAAGCTGAAGAGAGTCTTTTCTGCACAAATCTCTCATGAGTCCAGCT	130		
Db	3933	TTTCTTTGATATAGAGGGGCGAGATTTGTTAGTCTTCATGTCCAAATGGCACCAT	3874		
QY	131	TCCTGGAAATGGTTGAAAAGCTGTGCCTCTCTCCCATCTCCCT	174		
Db	3873	GCCCCACATTTTCAGTTTTTTAGGTCAGGAGGCTCTCTTCATTTTCTT	3830		

RESULT 14
 US-08-646-715-10/c
 ; Sequence 10, Application US/08646715
 ; Patent No. 5637686
 ; GENERAL INFORMATION:
 ; APPLICANT: Tjian, Robert
 ; APPLICANT: Comai, Lucio
 ; APPLICANT: Dynlacht, Brian D.
 ; APPLICANT: Hoey, Timothy
 ; APPLICANT: Rupprecht, Siegfried
 ; APPLICANT: Tanese, Naoko
 ; APPLICANT: Wang, Edith
 ; APPLICANT: Weizsaecker, Robert O.J.
 ; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
 ; NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/646,715
 ; FILING DATE: 09-MAY-1996

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,582
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-57650-2/AUT/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5962 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..5692
;
US-08-646-715-10

Query Match 12.0%; Score 28; DB 1; Length 5962;
Best Local Similarity 48.2%; Pred. No. 16;
Matches 79; Conservative 0; Mismatches 85; Indels 0; Gaps 0

QY 11 GCGTGCOCCTTGTCTCTCTCTTGACCCCTCTTGGCAGCTCACATGGACAAGGCCGGGTA 70
DB 3993 GTCCTTTTCCAACTCCTCTCTCTCTGTCTGTCTGCAACAGGGTTGGAAAGTGGCGCA 3934

QY 71 TGACTTTGCACTGAGCTGAAGGAGCTCTTTTCTGACAATTTCTCTCATGATGCCAGCT 130
DB 3933 TTTGTTTGAATATAGAGGGGGGAGAAATTTGTAGTCTCTCTGTTGCAATGGCACCACAT 3874

QY 131 TCCCTGGAATGCTTGAAAGCTCTGCTCTCTCCCTCCCATCTCCCT 174
DB 3873 GCCCACCATTTCAGTTTTTATGCTTCAGGAGCGCTCTTCATTTTCTT 3830

```

RESULT 15
US-08-937-466-1/c
; Sequence 1, Application US/08937466
; Patent No. 5846779
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ning
; APPLICANT: Amaral, M. Catherine
; APPLICANT: Chen, Jin-Long
; TITLE OF INVENTION: UCP3 Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,466
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341

```

; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2782 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-937-466-1

Query Match      11.9%; Score 27.8; DB 2; Length 2782;
Best Local Similarity 53.2%; Pred. No. 14;
Matches 59; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 56 GAACAGGCGCGGTATGACTTGGCACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCT 115
Db 2101 GAAACCTCCGAGAGAGAGCGCAGAGAGAGCTGTCTCTGCGCCCTAAGGTGGAG 2042

QY 116 CCTATGAGTCCAGCTTCTCGAATTGCTTGAAAAGCTCTGCTCTCCTCCTCC 166
Db 2041 ATTCTGAGTCTGCTGCTTTGAACTGATGACAGGCGAGTGCCCCCCCCCCC 1991

Search completed: May 1, 2003, 05:14:21
Job time : 99.449 secs

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GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
Run on: May 1, 2003, 03:08:45 ; Search time 1171.86 Seconds
(without alignments)
3233.964 Million cell updates/sec

Title: US-09-092-296-7_COPY_51_284
Perfect score: 234
Sequence: 1 ATGGGGCTGGGCTGCCCT.....ACCATGTTGTCGACACACA 234

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estom:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	234	100.0	456	12	BG506690 601861290
c 2	232.4	99.3	449	10	AW293443 UI-H-B12
3	232.4	99.3	830	13	BI759796 603045679
c 4	221	94.4	422	12	BF002050 7998c11.x
5	194.2	83.0	895	13	BI820029 603037210
6	181.2	77.4	865	13	BI820110 603037110

c	7	175	74.8	404	9	AI857998	AI857998 wj69b01.x
8	117	50.0	361	12	BF521842	BF521842 UI-R-C2P-	
9	113.8	48.6	521	10	BB533837	BB533837 BB533837	
10	113.8	48.6	522	10	BB664284	BB664284 BB664284	
c	11	93.2	39.8	328	9	AI136523	AI136523 UI-R-C2P-
c	12	81.4	34.8	244	12	BF511043	BF511043 UI-H-B14-
c	13	75.8	32.4	552	17	AO718761	AO718761 HS-5511-B
c	14	47.6	20.3	633	17	AZ079350	AZ079350 RFCI-23-4
c	15	47.4	20.3	506	17	AZ241329	AZ241329 RRCI-23-7
c	16	37	15.8	496	12	BF920882	BF920882 RRCI-23-7
c	17	36.4	15.6	331	9	AA282040	AA282040 RRCI-23-7
c	18	36.4	15.6	365	10	AW263952	AW263952 RRCI-23-7
c	19	36.4	15.6	402	9	AA936790	AA936790 z89a901.x
c	20	36.4	15.6	424	9	AA741185	AA741185 z89a901.x
c	21	36.4	15.6	494	9	AA534569	AA534569 oh89a02.s
c	22	36.4	15.6	529	9	AI018775	AI018775 oh89a02.s
c	23	36.4	15.6	606	10	AW970327	AW970327 oh89a02.s
c	24	36.4	15.6	719	10	AW970246	AW970246 oh89a02.s
c	25	36.4	15.6	797	14	BQ775963	BQ775963 oh89a02.s
c	26	36.2	15.5	600	12	BG803137	BG803137 oh89a02.s
c	27	35.2	15.0	458	13	BJ231120	BJ231120 oh89a02.s
28	35.2	15.0	574	13	BJ254868	BJ254868 oh89a02.s	
29	35.2	15.0	729	13	BJ254605	BJ254605 oh89a02.s	
c	30	34.8	14.9	451	9	AI829206	AI829206 oh89a02.s
c	31	34.8	14.9	639	17	AG048646	AG048646 oh89a02.s
c	32	34.6	14.8	261	10	BB411111	BB411111 oh89a02.s
c	33	34.2	14.6	863	12	BG698056	BG698056 oh89a02.s
c	34	34	14.5	190	9	AI010074	AI010074 oh89a02.s
c	35	34	14.5	575	17	BH729561	BH729561 oh89a02.s
c	36	34	14.5	919	14	BQ2828365	BQ2828365 oh89a02.s
c	37	33.8	14.4	826	13	BI080794	BI080794 oh89a02.s
c	38	33.6	14.4	791	17	CNS03JMS	CNS03JMS oh89a02.s
c	39	33.4	14.3	545	14	T41524	T41524 oh89a02.s
c	40	33.4	14.3	550	12	BF779666	BF779666 oh89a02.s
c	41	33.2	14.2	282	9	AA991822	AA991822 oh89a02.s
c	42	33.2	14.2	597	10	AW013553	AW013553 oh89a02.s
c	43	33.2	14.2	740	17	AG135659	AG135659 oh89a02.s
c	44	33	14.1	803	17	BH440024	BH440024 oh89a02.s
c	45	33	14.1	827	17	BH712332	BH712332 oh89a02.s

ALIGNMENTS

RESULT 1
BG506690
LOCUS 601861290F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4070759 5', linear EST 27-MAR-2001
DEFINITION mRNA sequence.
ACCESSION BG506690.1 GI:13468207
VERSION EST.
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 456)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LICW915 row: d column: 24
High quality sequence stop: 401.
Location/Qualifiers

source

1..456

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4070759"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phase-resistant)"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggcgctcgcc); Site:2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATGAGGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGGACATG-dr(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BASE COUNT 109 a 137 c 106 g 103 t
ORIGIN
Query Match 100.0%; Score 234; DB 12; Length 456;
Best Local Similarity 100.0%; Pred. No. 5.3e-55;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGGTCTGGGCTGCCCTTGTCTCTTGACCTCTTGCCCTTGCGAGCTCACATGGAACA 60
Db 45 ATGGGGTCTGGGCTGCCCTTGTCTCTTGACCTCTTGCCCTTGCGAGCTCACATGGAACA 104
QY 61 GGGCGGGTATGACTTTCGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 120
Db 105 GGGCGGGTATGACTTTCGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 164
QY 121 GAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTGCCCTCCCTCCATCCTCCCTTCAGGG 180
Db 165 GAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTGCCCTCCCTCCATCCTCCCTTCAGGG 224
QY 181 ACCAGCTGACCTCCACATGCAAGATCTCACACCATGTGTCGCAACACA 234
Db 225 ACCAGCTGACCTCCACATGCAAGATCTCACACCATGTGTCGCAACACA 278

RESULT 2
AW293443/c 449 bp mRNA linear EST 16-JAN-2000
LOCUS UI-H-BI2-ahm-c-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
DEFINITION IMAGE:2727182 3', mRNA sequence.
ACCESSION AW293443
VERSION AW293443.1 GI:6700079
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 449)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cyraps-remail.nih.gov
The sequence contained an oligo-dr track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CCAP clone distribution information can be found through the
I.M.A.G.E. Consortium/JLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1. .449
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2727182"
/clone_lib="NCI_CGAP_Sub4"
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/lab_host="DH10B (Life Technologies)"
/notes="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site:1: Not I; Site:2: Eco RI; The
NCI_CGAP_Sub4 library is a subtracted library derived from
the NCI_CGAP_Sub2 library which is a subtracted library
derived from the NCI_CGAP_Sub1 library, which is a
subtracted library derived from BI. BI constitutes a
mixture of 21 normalized or subtracted NCI_CGAP
libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28,
NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5,
NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11,
NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_Cu11,
NCI_CGAP_Lu2, NCI_CGAP_Brn23, NCI_CGAP_Lu5,
NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_Gc4, NCI_CGAP_Gc6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 : LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE Clonids 1322376-1323911,
1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 :
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonids
1323912-1325831, 1471368-1472903, 1492104-1493255)
NCI_CGAP_Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE
Clonids 1414920-1417991, 1520904-1522439) NCI_CGAP_Gc4
pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
Clonids 1257096-1258631, 1469064-1470983, 1475592-1476743)
NCI_CGAP_Pr22 pool 1 : LLAM 2457-2459, 2758-2759,
3062-3068 (IMAGE Clonids 985608-986759, 1101192-1101959,
1217928-1220615) NCI_CGAP_Co10 pool 1 : LLAM 2644-2653,
2871-2872 (IMAGE Clonids 1057416-1061255, 1144584-1145351)
) Subtraction was performed as previously described
(Bonaldi, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
Genome Research 6, 791-806.)
TAG_LIB=NCI_CGAP_Co4
TAG_TISSUE=colon
TAG_SEQ=CTCG"
BASE COUNT 104 a 108 c 134 g 103 t
ORIGIN
Query Match 99.3%; Score 232.4; DB 10; Length 449;
Best Local Similarity 99.6%; Pred. No. 1.5e-54;
Matches 233; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGGTCTGGGCTGCCCTTGTCTCTTGACCTCTTGCGAGCTCACATGGAACA 60
Db 387 ATGGGGTCTGGGCTGCCCTTGTCTCTTGACCTCTTGCGAGCTCACATGGAACA 328
QY 61 GGGCGGGTATGACTTTCGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 120
Db 327 GGGCGGGTATGACTTTCGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 268
QY 121 GAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTGCCCTCCCTCCATCCTCCCTCAGGG 180
Db 267 GAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTGCCCTCCCTCCATCCTCCCTCAGGG 208
QY 181 ACCAGCTGACCTCCACCATGCAAGATCTCACACCATGTGTCGCAACACA 234
Db 207 ACCAGCTGACCTCCACCATGCAAGATCTCACACCATGTGTCGCAACACA 154

RESULT 3
BI759796 830 bp mRNA linear EST 25-SEP-2001
LOCUS 603045679F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186107 5',
DEFINITION mRNA sequence.
ACCESSION BI759796
VERSION BI759796.1 GI:15751374
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 830)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11464 row: m column: 20
High quality sequence stop: 432.
Location/Qualifiers
1. 830
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5186107"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCW-SF0R6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
BASE COUNT 175 a 276 c 210 g 168 t 1 others
ORIGIN

Query Match 99.3%; Score 232.4; DB 13; Length 830;
Best Local Similarity 99.6%; Pred. No. 2e-54;
Matches 233; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGCTGGGCTGCCCTTGTCTCTTGTGACCTCTTGGCAGCTCACATGGAACA 60
Db 81 ATGGGCTGGGCTGCCCTTGTCTCTTGTGACCTCTTGGCAGCTCACATGGAACA 140
Qy 61 GGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTTCACAAATTCCTCTAT 120
Db 141 GGACCGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTTCACAAATTCCTCTAT 200
Qy 121 GAGTCCAGCTTCCTGGAAATGCTTGAAGAAGCTGTGCTCTCTCTCCATCTCCCTTCAGG 180
Db 201 GAGTCCAGCTTCCTGGAAATGCTTGAAGAAGCTGTGCTCTCTCTCCATCTCCCTTCAGG 260
Qy 181 ACCAGGTCACCTCCACCATCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 261 ACCAGGTCACCTCCACCATCAAGATCTCAACACCATGTTGTCTGCAACACA 314

RESULT 4
LOCUS BF002050/c 422 bp mRNA linear EST 06-OCT-2000
DEFINITION 7996cl1.x1 NCI_CGAP_Col16 Homo sapiens cDNA clone IMAGE:3314516 3', mRNA sequence.
ACCESSION BF002050
VERSION BF002050.1 GI:10702325
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 422)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -400P from Gibco.
Location/Qualifiers
1. 422
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3314516"
/clone_lib="NCI_CGAP_Col16"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: p77T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Col10 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1057416-1061255, and 1144584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 102 a 99 c 130 g 88 t 3 others
ORIGIN

Query Match 94.4%; Score 221; DB 12; Length 422;
Best Local Similarity 98.7%; Pred. No. 2.2e-51;
Matches 232; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 ATGGGGTCTGGGCTGCCCTTGTCTCTTGTGACCTCTTGGCAGCTCACATGGAACA 60
Db 377 ATGGGGTCTGGGCTGCCCTTGTCTCTTGTGACCTCTTGGCAGCTCACATGGAACA 318
Qy 61 GGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTTCACAAATTCCTCTAT 120
Db 317 GGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTTCACAAATTCCTCTAT 258
Qy 121 GAGTCCAGCTTCCTGGAAATGCTTGAAGAAGCTGTGCTCTCTCCATCTCCCTTCAGG 179
Db 257 GAGTCCAGCTTCCTGGAAATGCTTGAAGAAGCTGTGCTCTCTCCATCTCCCTTCAGG 198
Qy 180 GACCAGCTCACCTCCACCATCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 197 GACCAGCTCACCTCCACCATCAAGATCTCAACACCATGTTGTCTGCAACACA 143

RESULT 5
LOCUS BI820029 895 bp mRNA linear EST 04-OCT-2001
DEFINITION 603037210F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178171 5', mRNA sequence.
ACCESSION BI820029
VERSION BI820029.1 GI:15931579
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 895)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM1444 row: c column: 04
 High quality sequence start: 5
 High quality sequence stop: 422.
 Location/Qualifiers
 1. .895
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5178171"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /notes="Organ: pooled brain, lung, testis; Vector:
 PCWV-SPORT6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 89. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

FEATURES
 source

BASE COUNT 349 a 229 c 202 g 115 t
 ORIGIN
 Query Match 83.08; Score 194.2; DB 13; Length 895;
 Best Local Similarity 98.5%; Pred. No. 9.7e-44;
 Matches 196; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 36 CCTCTTGGCAGCTCACATGGAACAGGCGGGTATGACTTTGCAACTGAAGCTGAAGGA 95
 Db 6 CCTCTTGGCAGCTCACATGGAACAGGCGGGTATGACTTTGCAACTGAAGCTGAAGGA 65
 QY 96 GTCTTTTCTGCAAAATTCCTCTATGAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTG 155
 Db 66 GTCTTTTCTGCAAAATTCCTCTATGAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTG 125
 QY 156 CCTCTCTCCATCTCCCTTCAGGACAGCGCTCACCTCCACATGCAAGATCTCAACA 215
 Db 126 CCTCTCTCCATCTCCCTTCAGGACAGCGCTCACCTCCACATGCAAGATCTCAACA 185
 QY 216 CCATGTTGCTGCAACACA 234
 Db 186 CCATGTTGCTGCAACACA 204

RESULT 6
 BI820110 865 bp mRNA linear EST 04-OCT-2001
 LOCUS 603037110F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178170 5',
 DEFINITION
 mRNA sequence.
 ACCESSION BI820110
 VERSION BI820110
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 865)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrived by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM1444 row: c column: 03
 High quality sequence stop: 417.
 Location/Qualifiers
 1. .865
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5178170"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /notes="Organ: pooled brain, lung, testis; Vector:
 PCWV-SPORT6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 89. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

FEATURES
 source

BASE COUNT 330 a 219 c 198 g 117 t
 ORIGIN
 Query Match 77.4%; Score 181.2; DB 13; Length 865;
 Best Local Similarity 97.5%; Pred. No. 4.1e-40;
 Matches 194; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 36 CCTCTTGGCAGCTCACATGGAACAGGCGGGTATGACTTTGCAACTGAAGCTGAAGGA 95
 Db 6 CCTCTTGGCAGCTCACATGGAACAGGCGGGTATGACTTTGCAACTGAAGCTGAAGGA 65
 QY 96 GTCTTTTCTGCAAAATTCCTCTATGAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTG 155
 Db 66 GTCTTTTCTGCAAAATTCCTCTATGAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTG 124
 QY 156 CCTCTCTCCATCTCCCTTCAGGACAGCGCTCACCTCCACATGCAAGATCTCAACA 215
 Db 125 CCTCTCTCCATCTCCCTTCAGGACAGCGCTCACCTCCACATGCAAGATCTCAACA 184
 QY 216 CCATGTTGCTGCAACACA 234
 Db 185 CCATGTTGCTGCAACACA 203

RESULT 7
 AI857998/c AI857998 404 bp mRNA linear EST 21-DEC-1999
 LOCUS w169b01.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408041 3',
 DEFINITION
 mRNA sequence.
 ACCESSION AI857998
 VERSION AI857998.1 GI:5511614
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 404)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrived by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 629 Std Error: 0.00

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Seq primer: -400P from Gibco
High quality sequence stop: 395.
Location/Qualifiers
1. .404

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2408041"
/clone_lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
metastatic)"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
pooled lung tumor tissue, and was then primed with a Not I
- Oligo(dT) primer. Double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p773 vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 97 a 105 c 117 g 84 t 1 others

Query Match 74.88; Score 175; DB 9; Length 404;
Best Local Similarity 99.4%; Pred. No. 1.6e-38;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 CAGGGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCGACAAATTCCT 118
Db 311 CAGGGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCGACAAATTCCT 252

QY 119 ATGAGTCCAGCTTCTGGAATCTTGAAGAGCTCGCTCCCTCCATCTCCCTTCAG 178
Db 251 ATGAGTCCAGCTTCTGGAATCTTGAAGAGCTCGCTCCCTCCATCTCCCTTCAG 192

QY 179 GGACGAGCTGACCTCCACCATGCAAGATCTCAACACCATGTGTGTCGAACACA 234
Db 191 GGACGAGCTGACCTCCACCATGCAAGATCTCAACACCATGTGTGTCGAACACA 136

RESULT 8
BF521842
LOCUS

DEFINITION
UI-R-C2p-nq-e-02-0-UI.r1 UI-R-C2p Rattus norvegicus cDNA clone

ACCESSION
BF521842
VERSION

KEYWORDS
BF521842.1 GI:11629809
EST.

SOURCE
Norway rat.
Rattus norvegicus

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 361)
Bonaldo, M.F., Lennon, G. and Soares, M.B.

AUTHORS
Normalization and subtraction: two approaches to facilitate gene
discovery

TITLE
Genome Res. 6 (9), 791-806 (1996)

JOURNAL
9704477

MEDLINE
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping

COMMENT
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 9560
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1792770
Seq primer: M13 Forward.

FEATURES
source

Location/Qualifiers
1. .361
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C2p-nq-e-02-0-UI"
/clone_lib="UI-R-C2p"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site1: Not I; Site2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996)"

BASE COUNT 79 a 121 c 91 g 70 t

Query Match 50.0%; Score 117; DB 12; Length 361;
Best Local Similarity 69.4%; Pred. No. 2.5e-22;
Matches 159; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 ATGGGGTCTGGGCTGCCCCCTTGTCTTGGACCTCTTGGCAGCTCACATGGGAACA 60
Db 22 ATGGAGCCTTCGATGCTGCTCTTCTCTGACCTCTCTGCGAGCTCTGCAAGGG 81

QY 61 GGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCGACAAATTCCTCTAT 120
Db 82 CCAACAAGGTGACTTTGCAAGTAAACTGACCGAGCATCTCAGGCCAAGACCTCCAA 141

QY 121 GAGTCCAGCTTCCTGGAAATGCTTGAAGCTCTGCTCTCTCCATCTCCCTTCAGGG 180
Db 142 GACTCCGGCTTCTGGACATGCTCCAAAAGATCTGCTCTCTCCACCTCTCACCGGG 201

QY 181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTGTGTCTGCA 229
Db 202 ACCAATGTCACTTCATCAATAAGGGCCACACACCATCTTACCTGCA 250

RESULT 9
BB533837
LOCUS

DEFINITION
BB533837 RIKEN full-length enriched, 0 day neonate lung Mus

ACCESSION
BB533837
VERSION

KEYWORDS
BB533837.2 GI:16446306
EST.

SOURCE
house mouse.
Mus musculus

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 521)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda,
M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sano, H., Sasaki

D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
On Jul 29, 2000 this sequence version replaced gi:9585766.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscl.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES
Source
1. 521
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="E030032D13"
/clone_lib="RIKEN full-length enriched, 0 day neonate lung"
/tissue_type="lung"
/dev_stage="0 day neonate"
/lab_host="DH10a"
/note="Site_1: Salt; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGACGGCCGCAACTCGAGTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGATCTCGAGTTAATTAATATCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." 119 a 163 c 125 g 114 t
BASE COUNT
ORIGIN
Query Match
48.6%; Score 113.8; DB 10; Length 521;

Best Local Similarity 71.6%; Pred. No. 2.3e-21;
Matches 164; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
Qy 1 ATGGGCTCTGGGCTGCCCTTGGCTCTCTCTTGGACCTCTTGGCAGCTCACATGGAA 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 174 ATGAGGCTCTTGAAGCGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 230
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 GGCCCGGGTATGACTTTTGCACCTGAAGCTGAAGGAGTCTTTTCTGACAAATCTCTCTAT 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 231 GGCCAAAGTGACTTTTGCAGGTAAAGCTGACCGAGACTTTTTCAGGACAAGACCTCCAG 290
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 GACTCAGCTTCTCGGAATCTTTGAAAGCTCTGCCTCTCTCTCTCTCTCTCTCTCTCT 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 291 AATCTCGTCTGGACATGCTCCAAAGATCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 350
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 ACCAGCGTCACTCCCTCCACCAAGATCTCAACACCATGTTCTCTGCA 229
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 351 ACCAATGTCACCTTCTTCAAAAGGACCACACACTACCTTTACTTGCA 399
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 10
BB664284 522 bp mRNA linear EST 26-OCT-2001
LOCUS BB664284 RIKEN full-length enriched, 0 day neonate lung Mus
DEFINITION musculus cDNA clone E030032D13 5', mRNA sequence.
ACCESSION BB664284
VERSION BB664284.1 GI:16498038
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 522)
REFERENCE
AUTHORS
Takahashi, F., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
TITLE
JOURNAL
COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscl.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

VERSION	BF511043.1	GI:11594341
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 244)	
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov The sequence contained an oligo-qt track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/image/image.html Seq primer: M13 Forward POLYA=Yes.	
FEATURES	Location/Qualifiers	
source	1..244	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:3087887"	
	/lab.lib="NCI-CGAP_Sub8"	
	/lab.host="DH10B (Life Technologies)"	
	/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; NCI-CGAP_Sub8 is a subtracted library derived from NCI-CGAP_Sub5. The NCI-CGAP_Sub8 library had 2.5 million recombinants. A single-stranded DNA preparation of NCI-CGAP_Sub5 was used as a tracer in a subtractive hybridization with a driver comprising: a pool of clones from NCI-CGAP_Sub5 (IMAGE clone ids 2732833-2737415, 3068040-3069191; 25% of the driver population), a pool of clones from NCI-CGAP_Sub4 (IMAGE clone ids 2723592-2729326; 25% of the driver population), NCI-CGAP_Sub6 (pool AIF-AJU, IMAGE ids 2728969-2733190; 25% of the driver population), and NCI-CGAP_Sub7 (IMAGE ids 3069192-3072238, 3081864-3084550; 25% of the driver population). Subtraction was performed as previously described [Bonaldo, Lemon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.	
	TAG_LIB=NCI-CGAP_Co4	
	TAG_TISSUE=colon	
	TAG_SEQ=CTTCG	
BASE COUNT	51 a 68 g 71 t	
ORIGIN		
	Query Match 34.8%; Score 81.4; DB 12; Length 244;	
	Best Local Similarity 93.4%; Pred. No. 1.9e-12;	
	Matches 85; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
Qy	144 TGAAGAAGCTCTGCCTCCTCCATCCATCCCTTCAGGACACGAGCTCACCTCACCATGC 203	
Db	244 TGAAGAAGCTGTACATCTCGTCCATCTCCCTTCAGGACAAAGAGTCCACCTCCACCATGC 185	
Qy	204 AGAGTCTCAACACATGTTGTTCTGCAACACA 234	
Db	184 AGAGTCTCAACACATGTTGTTCTGCAACACA 154	
RESULT 13		
LOCUS	AQ1718761	552 bp DNA linear GSS 13-JUL-1999
DEFINITION	HS_5511_B2_F09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1087 Col=18 Row=L, DNA sequence.	
ACCESSION	AQ1718761	
VERSION	AQ1718761.1	GI:5468077

GSS.	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 552)	
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.	
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)	
MEDLINE	99380589	
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 1087 row: L column: 18 Seq primer: T7 Class: BAC ends High quality sequence stop: 552.	
FEATURES	Location/Qualifiers	
source	1..552	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="Plate=1087 Col=18 Row=L"	
	/clone.lib="RPCI-11 Human Male BAC Library"	
	/sex="male"	
	/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"	
BASE COUNT	141 a 153 c 124 g 117 t	
ORIGIN		
	Query Match 32.4%; Score 75.8; DB 17; Length 552;	
	Best Local Similarity 86.3%; Pred. No. 1e-10;	
	Matches 83; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
Qy	57 AACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTC 116	
Db	474 AGCATGCGAGGTATGACTTTGCACTGAAGCTGAAGAGTCTATTATGACAAATTCGTC 415	
Qy	117 CTATGAGTCCAGCTTCCTCGGAATTCGTTGAAAAGCT 152	
Db	414 TTATGAGTCCAGCTTCCTCGGAATTCGTTGAAAAGT 379	
RESULT 14		
LOCUS	AZ079350/c	633 bp DNA linear GSS 31-MAR-2000
DEFINITION	RPCI-23-438H19.TV RPCI-23 Mus musculus genomic clone RPCI-23-438H19 , DNA sequence.	
ACCESSION	AZ079350	
VERSION	AZ079350.1	GI:7372249
KEYWORDS	house mouse.	
SOURCE	Mus musculus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 633)	
REFERENCE	Zhao,S., Nlerman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret ,B., Levins,M., McGann,S., Tsegay,G, Geer,K., Krol,M., de Jong,	

Clones are derived from the mouse BAC library RC1-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 438 row: H column: 19
 Seq primer: T7
 Class: BAC ends.

```

/sex="Female"
/lab_host="DH10B"
/notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
ECORI; Site_2: ECGRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECGRI and ECGRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
116 a 145 c 138 g 107 t
BASE COUNT

```

	Matches	60: Conservative	0: Mismatches	21: Indels	0: Gaps	0:
QY	149	AGCTCTGCCCTCCCTCCATCTCCCTTCAGGACACAGGTCACCCCTCCACCATGCAAGAT	208			
Db	174	AGATCTGCTCTCTCTCCATCTGCGCATGCGGACCAATGTACCCCTCTTTCACAAAGGAC	115			
QY	209	CTCAACACCATGTTGCTGCA	229			
Db	114	CACCACACTACTTACTTGA	94			

GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:59:25 ; Search time 765,143 Seconds
(without alignments)
8900.373 Million cell updates/sec

Title: US-09-092-296-7_COPY_51_284
Perfect score: 234
Sequence: 1 AAGGGCTGGGTGCCCCCT.....ACCAAGTGTGTCGCAACACA 234

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2034640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rtd.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	234	100.0	422	6	AX092334	Sequence
2	234	100.0	422	6	AX376174	Sequence
3	234	100.0	422	6	AX403475	Sequence
4	232.4	99.3	484	6	AY102070	Homo sapi
5	176	75.2	624	6	AX472955	Sequence
6	92.4	39.5	47323	9	AC005937	Homo sapi
7	92.4	39.5	104154	2	AL773541	Homo sapi
8	92.4	39.5	156272	9	AL669830	Human DNA
9	92.4	39.5	178688	2	AL713893	Homo sapi
10	92.4	39.5	192650	9	AB023048	Homo sapi
11	92.4	39.5	200000	9	AP000511	Homo sapi
12	90.8	38.8	84474	9	AL662854	Human DNA
13	68.4	29.2	349980	6	AX344553	Sequence
14	68.4	29.2	349980	6	AX344554	Sequence
15	62.6	26.8	349980	6	AX344571	Sequence
16	48.4	20.7	132977	2	RN510020	Sequence
17	48.4	20.7	337832	2	AC099175	Rattus no
18	46	19.7	175345	2	AC022301	Mus muscu
19	37.8	16.2	185154	2	AC127110	Rattus no
20	37	15.8	168145	9	AL159171	Human DNA
21	36.8	15.7	2649	5	AF282675	Danio rer
22	36.4	15.6	118276	9	AC004148	Homo sapi
23	36	15.4	155406	2	AC105514	Rattus no
24	35.6	15.2	187533	2	AC125827	Rattus no
25	35.4	15.1	145253	9	AC006329	Homo sapi
26	35	15.0	67243	2	AC100215	Mus muscu
27	35	15.0	289157	2	AC103283	Rattus no
28	34.8	14.9	157104	9	AC108686	Homo sapi
29	34.8	14.9	161973	2	AC115067	Mus muscu
30	34.8	14.9	172421	2	AL683803	Mus muscu
31	34.8	14.9	182199	2	AC095097	Rattus no
32	34.8	14.9	193110	2	AC109311	Mus muscu
33	34.8	14.9	196491	9	AC092832	Homo sapi
34	34.6	14.8	88176	2	AL390202_09	Continuation (10 o
35	34.6	14.8	110275	10	AL663028	Mouse DNA
36	34.6	14.8	152502	2	AC012583	Homo sapi
37	34.6	14.8	170970	9	AL354707	Human DNA
38	34.2	14.6	3626	10	D86631	Mus sp. DNA
39	34.2	14.6	169197	2	AC115874	Mus muscu
40	34.2	14.6	190180	2	AC110539	Mus muscu
41	34	14.5	54472	2	AC122764	Mus muscu
42	34	14.5	211118	2	AC073752	Mus muscu
43	33.8	14.4	166991	2	AC102934	Mus muscu
44	33.8	14.4	174264	10	AL591373	Mouse DNA
45	33.8	14.4	175279	2	AC122589	Rattus no

ALIGNMENTS

RESULT 1
AX092334
LOCUS AX092334
DEFINITION Sequence 65 from Patent WO0116318.
ACCESSION AX092334
VERSION AX092334.1 GI:13444481
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 422)
Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.

variation		47240..47256	/note="clonal variation with 3' overlapping clone - insertion of 17bp repeat"
BASE COUNT	11556 a 11489 c 12284 g 11994 t		
ORIGIN			
Query Match			
Best Local Similarity 39.5%; Score 92.4; DB 9; Length 47323;			
Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY 59 CAGGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCT 118			
Db 35465 CAGGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCT 35524			
QY 119 ATGAGTCAGCTTCCTGGAATTCCTTGAAGCT 152			
Db 35525 ATGAGTCAGCTTCCTGGAATTCCTTGAAGGT 35558			
RESULT 7			
AL773541	104154 bp	DNA	linear
LOCUS	Homo sapiens chromosome 6 clone Xxbac-11J22, *** SEQUENCING IN		
DEFINITION	PROGRESS ***, in ordered pieces.		
ACCESSION	AL773541		
VERSION	AL773541.4	GI:22204637	
KEYWORDS	HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 104154)		
JOURNAL	Direct Submission		
COMMENT	Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 11, 2002 this sequence version replaced gi:21621737.		
----- Genome Center -----			
Center: Wellcome Trust Sanger Institute			
Center code: SC			
Web site: http://www.sanger.ac.uk			
Contact: humquery@sanger.ac.uk			
----- Project Information -----			
Center project name: bqblj22			
----- Summary Statistics -----			
Assembly program: XGAP4; version 4.5			
Chemistry: Dye-terminator; 100% of reads			
Consensus quality: 104135 bases at least Q40			
Consensus quality: 104142 bases at least Q30			
Consensus quality: 104145 bases at least Q20			
Insert size: 104154; sum-of-contigs			
Insert size: 110727; 1.1% error; agarose-fp			
Quality coverage: 19.52x in Q20 bases; sum-of-contigs Quality			
coverage: 18.64x in Q20 bases; agarose-fp			

* NOTE: This is a 'working draft' sequence.			
* This sequence will be replaced			
* by the finished sequence as soon as it is available and			
* the accession number will be preserved.			
FEATURES	Location/Qualifiers		
source	1..104154		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/chromosome="6"		
	/clone="Xxbac-11J22"		
	/clone_lib="DNA-arts-BAC.1-QBL.1"		
	1..104154		
misc_feature	1..104154		
	/note="assembly fragment:00090"		
BASE COUNT	26560 a 25418 c 26093 g 26083 t		
ORIGIN			
Query Match		39.5%; Score 92.4; DB 2; Length 104154;	

Best Local Similarity 98.9%; Pred. No. 9.7e-18;
Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 CAGGGCCGGTATGACTTTCGAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCT 118
|||||
Db 67846 CAGGGCCGGTATGACTTTCGAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCT 67905
|||||

QY 119 ATGAGTCCAGCTTCTCGAATTCGTAAGAAAGCT 152

Db 67906 ATGAGTCCAGCTTCTCGAATTCGTAAGAAAGT 67939
|||||

RESULT 8
AL669830/c
LOCUS
DEFINITION
AL669830
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Human DNA sequence from clone XXbac-118E17 on chromosome 6,
complete sequence.

AL669830.9 GI:20135762

HTG.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Johnson, C.

Direct Submission

Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Apr 10, 2002 this sequence version replaced gi:20067510.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em., EMBL; Sw.,

SWISSPROT; Ir., TrEMBL; Wp., WormPEP; Information on the WormPEP

database can be found at

http://www.sanger.ac.uk/projects/C.elegans/wormpep

from a CHORI-501 human bac - PGF cell line library VECTOR:

PTARBAC2.1

This sequence was generated from part of bacterial clone contigs

constructed by the MHC Haplotype Consortium and collaborators.

Further information can be found at

http://www.sanger.ac.uk/HGP/Chr6/MHC.

Location/Qualifiers

1..156272

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/clone="XXbac-118E17"

/clone_lib="CHORI-501"

BASE COUNT 41135 a 37989 c 36907 g 40241 t

ORIGIN

Query Match 39.5%; Score 92.4; DB 9; Length 156272;

Best Local Similarity 98.9%; Pred. No. 9.9e-18;

QY 119 ATGAGTCCAGCTTCTCGAATTCGTAAGAAAGCT 152
|||||
Db 25498 ATGAGTCCAGCTTCTCGAATTCGTAAGAAAGT 25465
|||||

RESULT 9

AL713893

LOCUS

DEFINITION

AL713893

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Sims, S.

Direct Submission

Submitted (26-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Mar 29, 2002 this sequence version replaced gi:19772907.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: bpg307M4

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 177277 bases at least Q40

Consensus quality: 17708 bases at least Q30

Consensus quality: 177956 bases at least Q20

Insert size: 178188; sum-of-contigs

Insert size: 192613; 0.9% error; agarose-fp

Quality coverage: 8.57x in Q20 bases; sum-of-contigs Quality

coverage: 8.00x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently

* consists of 6 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved

1 37410: contig of 37410 bp in length

37411 37510: gap of 100 bp

37511 82372: contig of 44862 bp in length

82373 82472: gap of 100 bp

82473 142457: contig of 59985 bp in length

142458 142557: gap of 100 bp

142558 152859: contig of 10302 bp in length

152860 152959: gap of 100 bp

152960 172054: contig of 19095 bp in length

172055 172154: gap of 100 bp

172155 178688: contig of 6534 bp in length.

FEATURES

source

1..178688

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/clone="XXbac-307M4"

/clone_lib="CHORI-501"

1..37410

/note="assembly_fragment:03218

fragment_chain:1"

37511..82372

/note="assembly_fragment:00918

misc_feature

misc_feature

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misc_feature      82473..142457
                  /note="assembly_fragment:03231
                  /fragment_chain:1"
misc_feature      142558..152859
                  /note="assembly_fragment:03008
                  /fragment_chain:1"
misc_feature      152960..172054
                  /note="assembly_fragment:04309
                  /fragment_chain:1"
misc_feature      172155..178688
                  /note="assembly_fragment:03507
                  /fragment_chain:1
                  clone_end:17
BASE COUNT      46316 a 40707 c 42166 g 48998 t 501 others
ORIGIN
Query Match      39.5%; Score 92.4; DB 2; Length 178688;
Best Local Similarity 98.9%; Pred. No. le-17;
Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 CAGGCGCGGTATGACTTTCGAAGCTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCCT 118
      |||||
Db 173795 CAGGCGCGGTATGACTTTCGAAGCTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCCT 173854
      |||||

QY 119 ATGAGTCCAGCTTCTCGAATTCGTTGAAAAGCT 152
      |||||
Db 173855 ATGAGTCCAGCTTCTCGAATTCGTTGAAAAGCT 173888
      |||||

RESULT 10
AB023048          192650 bp DNA linear PRI 20-NOV-1999
LOCUS             Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
DEFINITION        clone:53L9, complete sequence.
ACCESSION         AB023048
VERSION           AB023048.1 GI:5672603
KEYWORDS          HTG.
SOURCE            Homo sapiens cell_line:978SK DNA, clone:53L9.
ORGANISM          Homo sapiens
REFERENCE         1 (sites)
AUTHORS           Shinya,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
                  Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
                  Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
                  Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
                  Bahram,S. and Inoko,H.
                  Molecular dynamics of MHC genesis unraveled by sequence analysis of
                  the 1,796,938-bp HLA class I region
JOURNAL           Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
MEDLINE           20027539
REFERENCE         2 (bases 1 to 192650)
AUTHORS           Shinya,T. and Takishima,N.
TITLE             Submitted (29-JAN-1999) Takashi Shinya, Tokai University School of
                  Medicine, Department of Molecular Life Science 2; Bohseidai,
                  Isehara, Kanagawa 259-1193, Japan
                  (E-mail:tsnlinaxis.icc.u-tokai.ac.jp, Tel:81-463-93-1121,
                  Fax:81-463-94-8884)
FEATURES           Location/Qualifiers
                    1..192650
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p21.3"
                     /clone="53L9"
BASE COUNT      49862 a 44743 c 45833 g 52212 t
ORIGIN
Query Match      39.5%; Score 92.4; DB 9; Length 192650;

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```

Best Local Similarity 98.9%; Pred. No. le-17;
Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 CAGGCGCGGTATGACTTTCGAAGCTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCCT 118
      |||||
Db 177979 CAGGCGCGGTATGACTTTCGAAGCTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCCT 178038
      |||||

QY 119 ATGAGTCCAGCTTCTCGAATTCGTTGAAAAGCT 152
      |||||
Db 178039 ATGAGTCCAGCTTCTCGAATTCGTTGAAAAGCT 178072
      |||||

RESULT 11
AF000511          200000 bp DNA linear PRI 22-AUG-2001
LOCUS             Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
DEFINITION        section 10/20.
ACCESSION         AP000511 BA000025
VERSION           AP000511.1 GI:5926698
KEYWORDS          Homo sapiens DNA.
SOURCE            Homo sapiens
ORGANISM          Homo sapiens
REFERENCE         1
AUTHORS           Shiina,S., Tamiya,G., Oka,A. and Inoko,H.
TITLE             Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region
JOURNAL           Published Only in Database (1999)
REFERENCE         2 (bases 1 to 200000)
AUTHORS           Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.
TITLE             Direct Submission
JOURNAL           Submitted (21-SEP-1999) Mika Hirakawa, Japan Science and Technology
                  Corporation (JST), Advanced Databases Department; 5-3, Yonbancho,
                  Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@tokyo.jst.go.jp,
                  URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
                  Fax:81-3-5214-8470)
                  This sequence is conducted by Tokai University as a JST sequencing
                  Team.
COMMENT           Principal Investigator: Hidetoshi Inoko Ph.D
                  Phone:81-463-93-1121, Fax:81-463-94-8884.
                  The sequence is submitted by Human Genome Sequencing in ALIS
                  project of JST
                  Japan Science and Technology Corporation (JST)
                  5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan
                  For further information about this sequences, please visit our
                  sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.
                  html) or send email to webmaster@www-alis.tokyo.jst.go.jp.
FEATURES           Location/Qualifiers
                    1..200000
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p21.3"
                     /108774..108864
                     /note="SHGC-12985:The location is between each flanking
                     site of PCR primers."
                     /db_xref="GDB:735268"
                     /115648..115906
                     /standard_name="D6S1898"
                     /note="WI-9418:The location is between each flanking site
                     of PCR primers."
                     /db_xref="GDB:678272"
                     /note="Cda0vh10:The location is between each flanking site
                     of PCR primers."
                     /db_xref="GDB:443382"
                     /127908..128284,128708..128786,128938..128985,
                     join(127993..128284,129767,129949..130081,130328..130411,
                     129637..129767,129949..130081,130328..130411,
                     130596..130664,130826..130937,131154..131242,
                     131334..131430,132032..132163,132556..132660,
                     132922..133061,133692..133813)
                     /gene="TFIIH"
gene

```


QY 59 CAGGCGGGTATGACTTGAACCTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCT 118
 Db 110306 CAGGCGGGTATGACTTGAACCTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCT 110365

QY 119 ATGAGTCCAGCTTCCTGGAATTCCTTGAAGAAGCT 152
 Db 110366 ATGAGTCCAGCTTCCTGGAATTCCTTGAAGAAGT 110399

RESULT 12
 LOCUS AL662854 84474 bp DNA linear PRI 24-APR-2002
 DEFINITION Human DNA sequence from clone Xbac-105N19 on chromosome 6,
 complete sequence.
 ACCESSION AL662854
 VERSION AL662854.7 GI:20068660
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Tracey A.
 TITLE Direct Submission
 JOURNAL Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Apr 7, 2002 this sequence version replaced gi:190311750.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em, EMBL; SW,
 SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
 database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep Xbac-105N19 is
 from a CHORI-502 human bac - COX cell line library VECTOR:
 PTABAC2.1
 This sequence was generated from part of bacterial clone contigs
 constructed by the MHC Haplotype Consortium and collaborators.
 Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr6/MHC.
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 Best Local Similarity 97.9%; Pred. No. 3e-17; Mismatches 0; Gaps 0;
 Matches 92; Conservative 0

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 DEFINITION Sequence 4 from Patent WO0200932.
 ACCESSION AX344553
 VERSION AX344553.1 GI:18492439
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
 TITLE Diagnosis of known genetic parameters within the mhc
 JOURNAL Patent: WO 0200932-A 4 03-JAN-2002;
 Epigenomics AG (DE)
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 BASE COUNT 86882 a 5859 c 85073 g 172166 t
 ORIGIN

Query Match 29.2%; Score 68.4; DB 6; Length 349980;
 Best Local Similarity 87.2%; Pred. No. 3.2e-10; Mismatches 11; Indels 0; Gaps 0;
 Matches 75; Conservative 0

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 Db 319291 AACTCTACCTCTCTCTCCATCTCCCTTCAAAAACCAAGCTCCACCTCCACCATGCAAAAT 319232

QY 209 CTCACACCATGTTCTGCAACACA 234
 Db 319231 CTCACACCATATTATTCACACACA 319206

RESULT 14
 LOCUS AX344554/c 349980 bp DNA linear PAT 01-FEB-2002
 DEFINITION Sequence 5 from Patent WO0200932.
 ACCESSION AX344554
 VERSION AX344554.1 GI:18492440
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
 TITLE Diagnosis of known genetic parameters within the mhc
 JOURNAL Patent: WO 0200932-A 5 03-JAN-2002;
 Epigenomics AG (DE)
 FEATURES
 Location/Qualifiers
 source
 1. 349980
 /organism="synthetic construct"
 /db_xref="taxon:32630"

GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:55:40 ; Search time 160.776 seconds
(without alignments)
3277.661 Million cell updates/sec

Title: US-09-092-296-7_COPY_51_284

Perfect score: 234

Sequence: 1 ATGGGGTCTGGGCTCCGCTT.....ACCATGTTGCTGCAACACA 234

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	234	100.0	422 21	AAZ65087 Membrane-bound pro
2	234	100.0	422 22	AAS46045 Human DNA encoding
3	234	100.0	422 22	AAF92090 Human PRO1098 cDNA
4	234	100.0	422 21	AAF44233 Human PRO1098 (UNQ
5	234	100.0	431 21	AAZ98124 Human signal pepti
6	234	100.0	439 20	AAV84366 Human stomach carc
7	176	75.2	624 24	ABK81818 DNA representing l
8	94.4	40.3	729 23	AAS65519 DNA encoding novel
c 9	36.4	15.6	1611 22	ABAI9667 Human nervous syst

c 10	36.4	15.6	1611	22	AAK86283 Human immune/haema
c 11	34.8	14.9	1146	21	AAC63412 Human secreted pro
c 12	33.4	14.3	550	21	AAC93727 Cat flea hindgut a
c 13	32.6	13.9	4885	22	AAS44656 Human full-length
c 14	32.2	13.8	27082	22	AAK70447 Human immune/haema
c 15	32	13.7	13216	22	AAAL05122 Human reproductive
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c 25	31.2	13.3	2902	22	AAS31927 Human liver associ
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c 27	31	13.2	398	24	ABL77487 Human ovarian can
c 28	31	13.2	1850	21	AAAS1383 Chromosome 16q tum
c 29	31	13.2	4824	24	ABK70289 Human lung cancer
c 30	31	13.2	6457	24	ABN96892 Gene #3390 used to
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c 36	30.6	13.1	437	24	ABL37309 Human colon tumour
c 37	30.6	13.1	464	21	AAZ96747 Nuclear transport
c 38	30.6	13.1	467	24	AAFL7906 Human ovarian can
c 39	30.6	13.1	565	21	AAF16146 Human prostate can
c 40	30.6	13.1	830	22	AAH07574 Human cDNA clone (
c 41	30.6	13.1	1958	22	AAH16559 Human cDNA sequenc
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c 45	30.2	12.9	590	22	AAK34852 Human bone marrow

ALIGNMENTS

RESULT 1
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ID AAZ65087 standard; cDNA; 422 BP.
AC AAZ65087;
XX
XX
XX
DT 05-APR-2000 (first entry)
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XX
DE Membrane-bound protein PRO1098 encoding cDNA.
XX
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999:
XX
XX
PF 02-JUN-1999; 99WO-US12252.
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
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PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
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 PR 20-JUL-1998; 98US-0093339.
 PR 30-JUL-1998; 98US-0094651.
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 PR 18-AUG-1998; 98US-0097022.
 PR 19-AUG-1998; 98US-0097141.
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 PR 26-AUG-1998; 98US-0097955.
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 PR 26-AUG-1998; 98US-0097974.
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 PR 26-AUG-1998; 98US-0097986.
 PR 26-AUG-1998; 98US-0098014.
 PR 31-AUG-1998; 98US-0098525.
 PR 16-SEP-1998; 98US-0100634.
 PR 12-JAN-1999; 99US-0115565.
 XX (GETH) GENENTECH INC.
 XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;
 XX WPT: 2000-072883/06.
 DR P-PSDB; AAY66741.
 XX Membrane-bound proteins and related nucleotide sequences -
 PT Claim 2; Fig 257; 822pp; English.
 PS The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be

CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.

XX Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 100.0%; Score 234; DB 21; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.5e-65;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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ID AA546045 standard; cDNA; 422 BP.

XX AC AA546045;

XX 18-DEC-2001 (first entry)

XX Human DNA encoding PRO polypeptide sequence #121.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.

XX Homo sapiens.

XX W0200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194469P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.

PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
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PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.

XX (GETH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;

XX Pan J, Smith V, Watanabe CK, Wood WL, Zhang Z;

XX WPI; 2001-602746/68.

XX P-PSDB; AA029144.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -

XX Claim 2; Fig 241; 774pp; English.

XX Sequences AA545925-AA546231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.

XX SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 100.0%; Score 234; DB 22; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.5e-65;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||||||
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QY 61 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 120
Db |||||||
118 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177
QY 121 GAGTCCAGCTTCTCGGAATGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 180
Db |||||||
178 GAGTCCAGCTTCTCGGAATGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 237
QY 181 ACCAGGTCACCTCCACCATGCAAGATCTCAACACCATGTTGCTGCAACACA 234
Db |||||||
238 ACCAGGTCACCTCCACCATGCAAGATCTCAACACCATGTTGCTGCAACACA 291

RESULT 3
AAF92090
ID AAF92090 standard; cDNA; 422 BP.

XX AC AAF92090;
XX DT 15-MAY-2001 (first entry)
XX DE Human PRO1098 cDNA.
XX KW Human; PRO protein; mapping; ss.

XX OS Homo sapiens.
XX PN WO200116318-A2.
XX PD 08-MAR-2001.

XX PF 24-AUG-2000; 2000WO-US23328.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 07-DEC-1999; 99US-0169495.
XX PR 09-DEC-1999; 99US-0170262.
XX PR 11-JAN-2000; 2000US-0175481.
XX PR 18-FEB-2000; 2000WO-US04341.
XX PR 18-FEB-2000; 2000WO-US04342.
XX PR 22-FEB-2000; 2000WO-US04414.
XX PR 01-MAR-2000; 2000WO-US05601.
XX PR 03-MAR-2000; 2000US-0187202.
XX PR 25-APR-2000; 2000US-0199397.
XX PR 22-MAY-2000; 2000WO-US14042.
XX PR 05-JUN-2000; 2000US-0209832.
XX PA (GETH) GENENTECH INC.

XX PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX WPI: 2001-183260/18.
XX DR P-PSDB; AAB87558.

XX PT Eighty four nucleic acids encoding PRO polypeptides, useful in
XX PT molecular biology, including use as hybridization probes, and in
XX PT chromosome and gene mapping.
XX PS Claim 2; Fig 65; 278pp; English.

XX CC The present sequence is the coding sequence for a human PRO polypeptide
XX CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
XX CC antagonists or anti-PRO antibodies are useful for preparation of a
XX CC medicament useful in the treatment of a condition which is responsive to
XX CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
XX CC protein may also be employed as molecular weight markers for protein
XX CC electrophoresis. The PRO coding sequence has applications in molecular
XX CC biology, including use as hybridisation probes, and in chromosome and
XX CC gene mapping.

XX SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 100.0%; Score 234; DB 22; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.5e-65;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGTCTGGGCTGCCCTTGTCTTCCCTTGACCTCTTGGCAGCTTCACATGGACA 60

Db 58 ATGGGGTCTGGGCTGCCCTTGTCTTCCCTTGACCTCTTGGCAGCTTCACATGGACA 117

QY 61 GGGCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 120

Db 118 GGGCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 177

QY 121 GAGTCCAGCTTCCTGGAAATGCTTGAAAAGCTCTGCTCCTCCTCATCTCCCTTCAGGG 180
Db 178 GAGTCCAGCTTCCTGGAAATGCTTGAAAAGCTCTGCTCCTCCTCATCTCCCTTCAGGG 237
QY 181 ACCAGGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTTCTGCAACACA 234
Db 238 ACCAGGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTTCTGCAACACA 291

RESULT 4
AAF44233
ID AAF44233 standard; cDNA; 422 BP.
XX AC AAF44233;
XX DT 02-APR-2001 (first entry)
XX DE Human PRO1098 (UNQ541) nucleotide sequence SEQ ID NO:362.
XX KW Human; secreted and transmembrane protein; PRO; cytostatic;
XX KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
XX KW diagnostic assay; ss.

XX OS Homo sapiens.
XX PN WO200073454-A1.
XX PD 07-DEC-2000.
XX PF 30-MAR-2000; 2000WO-US08439.

XX PR 02-JUN-1999; 99WO-US12252.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 07-JUL-1999; 99US-0143048.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 28-JUL-1999; 99US-0146222.
XX PR 17-AUG-1999; 99US-0149396.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 15-SEP-1999; 99WO-US21547.
XX PR 08-OCT-1999; 99US-0158663.
XX PR 30-NOV-1999; 99WO-US28313.
XX PR 01-DEC-1999; 99WO-US28301.
XX PR 16-DEC-1999; 99WO-US30095.
XX PR 20-DEC-1999; 99WO-US30911.
XX PR 05-JAN-2000; 2000WO-US00219.
XX PR 06-JAN-2000; 2000WO-US00376.
XX PR 11-FEB-2000; 2000WO-US03565.
XX PR 18-FEB-2000; 2000WO-US04341.
XX PR 22-FEB-2000; 2000WO-US04414.
XX PR 24-FEB-2000; 2000WO-US04914.
XX PR 02-MAR-2000; 2000WO-US05004.
XX PR 15-MAR-2000; 2000WO-US05841.
XX PR 20-MAR-2000; 2000WO-US06884.
XX PR 20-MAR-2000; 2000WO-US07377.

XX PA (GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
XX PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX PI Zhang Z;
XX WPI: 2001-032160/04.
XX DR P-PSDB; AAB65264.
XX PT PRO polynucleotides used to produce polypeptides used to target
XX PT bioactive molecules such as toxins, radiolabels or antibodies, to
XX PT specific cells, to cause targeted cell death -
XX Claim 2; Fig 257; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;
 Query Match 100.0%; Score 234; DB 22; Length 422;
 Best Local Similarity 100.0%; Pred. No. 2.5e-65;
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGGGTCTGGGTCGCCCTTGTCTCTCTGTGACCTCTTGGCAGCTCACATGAACA 60
 DB 58 ATGGGGTCTGGGTCGCCCTTGTCTCTCTGTGACCTCTTGGCAGCTCACATGAACA 117
 QY 61 GGGCGGGTATGACTTTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 120
 DB 118 GGGCGGGTATGACTTTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 177
 QY 121 GAGTCAGCTTCTCGAATGCTTGAAGCTGTGCTCTCTCTCTCTCTCTCTCTCTAT 180
 DB 178 GAGTCAGCTTCTCGAATGCTTGAAGCTGTGCTCTCTCTCTCTCTCTCTCTAT 237
 QY 181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
 DB 238 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291
 RESULT 5
 AA298124
 ID AA298124 standard; cDNA; 431 BP.
 AC AA298124;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE Human signal peptide containing protein HSPP-16 cDNA SEQ ID NO:150.
 XX
 KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14484.
 XX
 PR 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX
 PA (INCY-) INCYTE PHARM INC.

XX
 PI Lal P, Tang YT, Gorgone CA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX
 DR WPI; 2000-160673/14.
 DR P-PSDB; AAY87239.
 XX
 XX New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease
 PT
 PS Claim 9; Page 261; 327pp; English.
 XX
 XX AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
 CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can
 CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPP. Antagonists of
 CC HSPP are used to treat or prevent disorders associated with increased
 CC activity or function of HSPP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
 CC nucleic acids can be used for the recombinant production of HSPP, for
 CC detecting HSPP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPP
 CC from natural sources.
 XX
 SQ Sequence 431 BP; 93 A; 135 C; 101 G; 102 T; 0 other;
 Query Match 100.0%; Score 234; DB 21; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.6e-65;
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGGGTCTGGGTCGCCCTTGTCTCTCTTGAACCTCTTGGCAGCTCACATGAACA 60
 DB 51 ATGGGGTCTGGGTCGCCCTTGTCTCTCTTGAACCTCTTGGCAGCTCACATGAACA 110
 QY 61 GGGCGGGTATGACTTTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 120
 DB 111 GGGCGGGTATGACTTTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 170
 QY 121 GAGTCAGCTTCTCGAATGCTTGAAGAGTCTGCTCTCTCTCTCTCTCTCTCTAT 180
 DB 171 GAGTCAGCTTCTCGAATGCTTGAAGAGTCTGCTCTCTCTCTCTCTCTCTCTAT 230
 QY 181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
 DB 231 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 284
 RESULT 6
 AAV84366
 ID AAV84366 standard; cDNA to mRNA; 439 BP.
 XX
 AC AAV84366;
 XX
 DT 30-MAR-1999 (first entry)
 XX
 DE Human stomach carcinoma cDNA clone HP10408.
 XX
 KW Transmembrane protein; HP10408; human; stomach cancer; ds.

```
XX OS Homo sapiens.
XX AC
XX FH Key Location/Qualifiers
XX FT CDS 75..311
XX FT /*tag= a
XX FT /note= "cDNA comprising the coding region (minus
XX FT the stop codon) is claimed (Claim 3)"
XX
XX PN WO9855508-A2.
XX XX
XX PD 10-DEC-1998.
XX XX
XX PF 03-JUN-1998; 98WO-JP02445.
XX XX
XX PR 03-JUN-1997; 97JP-0144948.
XX XX
XX PA (PROT-) PROTEGENE INC.
XX PA (SAGA ) SAGAMI CHEM RES CENTRE.
XX PI Kato S, Sekine S, Yamaguchi T;
XX WPI; 1999-045730/04..
XX DR P-PSDB; AAW88498.
XX
XX New human proteins containing transmembrane domains and their
XX encoding sequences - useful in the preparation of antibodies and
XX large-scale protein production, gene diagnosis, and gene therapy
XX
XX Claim 4; Page 135; 178pp; English.
XX
XX This is the nucleotide sequence of cDNA clone HP10408, which
XX includes a coding region (also claimed). The clone was isolated from a
XX transmembrane protein (see AAW88498). The clone was isolated from a
XX stomach cancer cDNA library using a signal sequence detection
XX method, and by protein synthesis by in vitro translation. The
XX encoded protein has a putative signal sequence and a putative
XX internal transmembrane domain. The invention provides nucleotide
XX sequences (see AAW84359-76) coding for 18 transmembrane proteins
XX (see AAW8491-508), vectors containing such polynucleotides, and
XX eukaryotic cells containing the vectors. The proteins can be
XX used as antigens or as compositions in the preparation of
XX antibodies against the proteins. The polynucleotides can be used
XX as probes for gene diagnosis, and as gene sources for gene therapy
XX and large-scale production of proteins encoded by the cDNA. The
XX host cells are used for the detection of ligands corresponding to
XX the expressed proteins, and the screening of low mol.wt. medicines.
XX
XX Sequence 439 BP; 89 A; 137 C; 109 G; 104 T; 0 other;
XX
Query Match 100.0%; Score 234; DB 20; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.6e-65;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGCTCGGCTGCCCTTCCTCTCTGACCTGAGGAGTCTTTTCTGACAAATTCCTCTAT 194
Db 75 ATGGGCTCGGCTGCCCTTCCTCTCTGACCTGAGGAGTCTTTTCTGACAAATTCCTCTAT 134
QY 61 GGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTAT 120
Db 135 GGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTAT 194
QY 121 GAGTCCAGCTTCCTGGATTCCTGAAAGCTCTGCCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 195 GAGTCCAGCTTCCTGGATTCCTGAAAGCTCTGCCTCTCTCTCTCTCTCTCTCTCTCTCT 254
QY 181 ACCAGGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 255 ACCAGGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 308
XX
RESULT 7
ABK81818
```

```
XX OS Homo sapiens.
XX AC
XX FH Key Location/Qualifiers
XX FT CDS 75..311
XX FT /*tag= a
XX FT /note= "cDNA comprising the coding region (minus
XX FT the stop codon) is claimed (Claim 3)"
XX
XX PN WO9855508-A2.
XX XX
XX PD 10-DEC-1998.
XX XX
XX PF 03-JUN-1998; 98WO-JP02445.
XX XX
XX PR 03-JUN-1997; 97JP-0144948.
XX XX
XX PA (PROT-) PROTEGENE INC.
XX PA (SAGA ) SAGAMI CHEM RES CENTRE.
XX PI Kato S, Sekine S, Yamaguchi T;
XX WPI; 1999-045730/04..
XX DR P-PSDB; AAW88498.
XX
XX New human proteins containing transmembrane domains and their
XX encoding sequences - useful in the preparation of antibodies and
XX large-scale protein production, gene diagnosis, and gene therapy
XX
XX Claim 4; Page 135; 178pp; English.
XX
XX This is the nucleotide sequence of cDNA clone HP10408, which
XX includes a coding region (also claimed). The clone was isolated from a
XX transmembrane protein (see AAW88498). The clone was isolated from a
XX stomach cancer cDNA library using a signal sequence detection
XX method, and by protein synthesis by in vitro translation. The
XX encoded protein has a putative signal sequence and a putative
XX internal transmembrane domain. The invention provides nucleotide
XX sequences (see AAW84359-76) coding for 18 transmembrane proteins
XX (see AAW8491-508), vectors containing such polynucleotides, and
XX eukaryotic cells containing the vectors. The proteins can be
XX used as antigens or as compositions in the preparation of
XX antibodies against the proteins. The polynucleotides can be used
XX as probes for gene diagnosis, and as gene sources for gene therapy
XX and large-scale production of proteins encoded by the cDNA. The
XX host cells are used for the detection of ligands corresponding to
XX the expressed proteins, and the screening of low mol.wt. medicines.
XX
XX Sequence 439 BP; 89 A; 137 C; 109 G; 104 T; 0 other;
XX
Query Match 100.0%; Score 234; DB 20; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.6e-65;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGCTCGGCTGCCCTTCCTCTCTGACCTGAGGAGTCTTTTCTGACAAATTCCTCTAT 194
Db 75 ATGGGCTCGGCTGCCCTTCCTCTCTGACCTGAGGAGTCTTTTCTGACAAATTCCTCTAT 134
QY 61 GGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTAT 120
Db 135 GGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTAT 194
QY 121 GAGTCCAGCTTCCTGGATTCCTGAAAGCTCTGCCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 195 GAGTCCAGCTTCCTGGATTCCTGAAAGCTCTGCCTCTCTCTCTCTCTCTCTCTCTCTCT 254
QY 181 ACCAGGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 255 ACCAGGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 308
XX
RESULT 7
ABK81818
```

```
ID ABK81818 standard; DNA; 624 BP.
XX AC
XX ABK81818;
XX DT 13-AUG-2002 (first entry)
XX DE DNA representing lung specific gene #4.
XX KW Lung specific gene; gene therapy; vaccine; lung cancer;
XX KW cancer staging; cancer monitoring; cancer diagnosis;
XX KW imaging lung cancer; metastases; gene; ss.
XX OS Homo sapiens.
XX PN WO200218576-A2.
XX PD 07-MAR-2002.
XX PF 27-AUG-2001; 2001WO-US26684.
XX PR 28-AUG-2000; 2000US-228378P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Chen S, Macina RA, Sun Y, Recipon H;
XX WPI; 2002-434904/46.
XX DR New lung specific genes and their encoded proteins, useful in gene
XX PT therapy or as a vaccine for treating lung cancer, as well as for
XX PT measuring metastases of lung cancer, or staging, monitoring, diagnosing
XX PT or imaging lung cancer -
XX PS Claim 1; Page 161; 206pp; English.
XX CC The invention describes a new lung specific gene and it's variants. The
XX CC lung specific gene proteins and genes are useful in gene therapy or as a
XX CC vaccine for treating lung cancer. Lung specific genes are also useful for
XX CC staging, monitoring, diagnosing or imaging lung cancer, as well as for
XX CC measuring metastases of lung cancer. This sequence represents a lung
XX CC specific gene described in the invention.
XX SQ Sequence 624 BP; 129 A; 175 C; 182 G; 138 T; 0 other;
XX
Query Match 75.2%; Score 176; DB 24; Length 624;
Best Local Similarity 100.0%; Pred. No. 1.4e-46;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 59 CAGGGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCT 118
Db 314 CAGGGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCT 373
QY 119 ATGAGTCCAGCTTCCTCGAATTGCTTGAAGAGCTCTGCCTCTCTCTCTCTCTCTCTCT 178
Db 374 ATGAGTCCAGCTTCCTCGAATTGCTTGAAGAGCTCTGCCTCTCTCTCTCTCTCTCTCT 433
QY 179 GGACCAAGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 434 GGACCAAGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 489
XX
RESULT 8
AAS65519
ID AAS65519 standard; cDNA; 729 BP.
XX AC
XX AAS65519;
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #1323.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
```


XX The invention relates to novel cat flea (*Ctenocephalides felis*) nucleic
CC acids which are expressed in hindgut and Malpighian tubule (HMT) tissue
CC or head and nerve cord (HNC) tissue. The invention also relates to the
CC encoded proteins. The invention additionally encompasses expression
CC constructs, recombinant viruses and recombinant cells comprising the
CC nucleic acids of the invention, recombinant production of the proteins,
CC the proteins, and compositions comprising the inhibitors of
CC administration to an animal. The nucleic acids, and the proteins they
CC encode may be used in the prevention, treatment and diagnosis of diseases
CC associated with flea infestations. For example, the nucleic acids may be
CC used to produce an HMT or HNC protein according to standard recombinant
CC DNA methodology by inserting the nucleic acids into a host cell and
CC culturing the cell to express the protein. The HMT and HNC nucleic acids
CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
CC and quantitate the presence of cat flea or other homologous nucleic acid
CC sequences in samples. They may also be used to study the expression and
CC function of the proteins and their role in metabolism. The HMT and HNC
CC proteins may be used as antigens in the production of specific
CC antibodies, and in assays to identify modulators (agonists and
CC antagonists) of HMT and/or HNC protein expression and activity. The
CC anti-HMT/HNC protein antibodies and antagonists may also be used to
CC downregulate protein expression and activity. The antibodies may also be
CC used as diagnostic agents for detecting the presence of flea polypeptides
CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
CC present sequence represents a cat flea HMT cDNA of the invention.
XX
SQ Sequence 550 BP; 153 A; 107 C; 144 G; 138 T; 8 other;

Query Match 14.3%; Score 33.4; DB 21; Length 550;
Best Local Similarity 58.6%; Pred. No. 1.1;
Matches 58; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 76 TTGCACACTAGCTGAGGAGTCTTTCTGCACAAATTCCTCTATGCTCCAGTCCCTG 135
DB 407 TTGTACACAGATGGTCATCTGGCGTTTGCAGACAGCGGCAATCTCTCCAGTGCCATT 348
QY 136 GAATTCGCTGAAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 174
DB 347 GCATCTGTAGCATCGTTCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 309

RESULT 13
AAS44656/C
ID AAS44656 standard; DNA; 4885 BP.
XX AAS44656;
AC
DT 18-DEC-2001 (first entry)
XX
XX Human full-length polynucleotide sequence #81.
XX Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW nervous system disorder; inflammatory disorder; cell differentiation; ds;
KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
KW cystic; antirheumatic; antiarthritic; vulnary; antiparkinsonian;
KW antibacterial; immunosuppressive; vasotropic; antiinflammatory;
KW neuroprotective; osteopathic; antidiabetic; antiashtmatic; antiallergic;
KW immunostimulant; analgesic; gene therapy.
XX
XX Homo sapiens.
XX
XX W0200164834-A2.
XX
XX 07-SEP-2001.
PD
XX 26-FEB-2001; 2001WO-US04926.
XX
XX 28-FEB-2000; 2000US-0515126.
PR

PR 18-MAY-2000; 2000US-0577409.
PR 17-JUN-2000; 2000US-0597707.
PR 14-JUL-2000; 2000US-0616807.
PR 19-SEP-2000; 2000US-0664641.
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
PI Dmanac R;
XX
XX WPI; 2001-589862/66.
DR P-PSDB; AAU27756.
XX
XX Novel polypeptides and nucleic acids obtained from cDNA libraries
XX prepared from various human tissues, for diagnosis, treatment of
XX cancer, neurological, inflammatory disorders and for use in arrays for
XX detection
XX
PS Claim 1; SEQ ID No 81; 153pp; English.
XX
XX Sequences AAS44576-AA544919 represent full-length polynucleotides and
XX contig polynucleotides encoding polypeptides of the invention. The DNA
XX and protein sequences are useful for the treatment, diagnosis and
XX prevention of various types of disorder in a mammalian subject such as a
XX human, dog, monkey, mouse, hamster or rat. The disorders include cancers
XX such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
XX as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
XX diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
XX disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
XX chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
XX Wernicke disease, inflammatory disorders such as nephritis, Crohn's
XX disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
XX bowel proliferation. The sequences exhibit activity relating to angiogenesis,
XX cell proliferation, cell differentiation stem cell growth factor,
XX activin or inhibin. Therefore, they can be used to manipulate stem cells
XX in culture to give rise to neuroepithelial cells that can be used to
XX augment or replace cells damaged by illness, accidental damage or genetic
XX disorders. The sequences may also be used for regeneration of bone,
XX cartilage, tendons and ligaments and in tissue repair and burn healing.
XX Note: Some sequences for this patent did not form part of the printed
XX specification, but were obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4885 BP; 1482 A; 920 C; 1159 G; 1324 T; 0 other;

Query Match 13.9%; Score 32.6; DB 22; Length 4885;
Best Local Similarity 51.7%; Pred. No. 5;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 59 CAGGGCGGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCT 118
DB 1268 CTGACCTGGCGCTGAGTTCACACTGAGTCTGAGAGCGGTTCTTTCTCTCTCTGCTGA 1209
QY 119 ATGAGTCCAGTCTCCCTGGAATTCCTGAAAGCTGCTGCTCTCTCTCTCTCTCTCTCA 178
DB 1208 CGAGATGCTGCTCTCTCCAGTTTCTTCGACGCGCTCCAGCTCTCTGCTGCTTTCG 1149
QY 179 GGACACCGAGTCACCCCTCCACCAT 201
DB 1148 TTGGGCGCTGGAGTCTCTTCAT 1126

RESULT 14
AAK70447
ID AAK70447 standard; DNA; 27082 BP.
XX
XX AAK70447;
AC
XX
XX 06-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25259.
DE
XX

KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;	25-SEP-2000; 2000US-0234997.	PR
KX	cytostatic; gene therapy; vaccine; metastasis; ds.	25-SEP-2000; 2000US-0234998.	PR
XX		26-SEP-2000; 2000US-0234984.	PR
OS	Homo sapiens.	27-SEP-2000; 2000US-0235834.	PR
XX		27-SEP-2000; 2000US-0235836.	PR
XX		29-SEP-2000; 2000US-0236327.	PR
PN	WO200157182-A2.	29-SEP-2000; 2000US-0236367.	PR
XX		29-SEP-2000; 2000US-0236368.	PR
XX		29-SEP-2000; 2000US-0236369.	PR
PD	09-AUG-2001.	29-SEP-2000; 2000US-0236370.	PR
PF	17-JAN-2001; 2001WO-US01354.	29-SEP-2000; 2000US-0236802.	PR
XX		02-OCT-2000; 2000US-0237037.	PR
XX		02-OCT-2000; 2000US-0237038.	PR
XX		02-OCT-2000; 2000US-0237039.	PR
PR		02-OCT-2000; 2000US-0237040.	PR
PR		13-OCT-2000; 2000US-0239935.	PR
PR		13-OCT-2000; 2000US-0239937.	PR
PR		20-OCT-2000; 2000US-0240960.	PR
PR		20-OCT-2000; 2000US-0241221.	PR
PR		20-OCT-2000; 2000US-0241785.	PR
PR		20-OCT-2000; 2000US-0241786.	PR
PR		20-OCT-2000; 2000US-0241787.	PR
PR		20-OCT-2000; 2000US-0241808.	PR
PR		20-OCT-2000; 2000US-0241809.	PR
PR		01-NOV-2000; 2000US-0241826.	PR
PR		01-NOV-2000; 2000US-0244617.	PR
PR		08-NOV-2000; 2000US-0246474.	PR
PR		08-NOV-2000; 2000US-0246475.	PR
PR		08-NOV-2000; 2000US-0246476.	PR
PR		08-NOV-2000; 2000US-0246477.	PR
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PR		08-NOV-2000; 2000US-0246524.	PR
PR		08-NOV-2000; 2000US-0246525.	PR
PR		08-NOV-2000; 2000US-0246526.	PR
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PR		08-NOV-2000; 2000US-0246528.	PR
PR		08-NOV-2000; 2000US-0246532.	PR
PR		08-NOV-2000; 2000US-0246609.	PR
PR		08-NOV-2000; 2000US-0246610.	PR
PR		08-NOV-2000; 2000US-0246611.	PR
PR		08-NOV-2000; 2000US-0246613.	PR
PR		17-NOV-2000; 2000US-0249207.	PR
PR		17-NOV-2000; 2000US-0249208.	PR
PR		17-NOV-2000; 2000US-0249209.	PR
PR		17-NOV-2000; 2000US-0249210.	PR
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PR		17-NOV-2000; 2000US-0249216.	PR
PR		17-NOV-2000; 2000US-0249217.	PR
PR		17-NOV-2000; 2000US-0249218.	PR
PR		17-NOV-2000; 2000US-0249244.	PR
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PR		17-NOV-2000; 2000US-0249265.	PR
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PR		17-NOV-2000; 2000US-0249300.	PR
PR		01-DEC-2000; 2000US-0250160.	PR
PR		01-DEC-2000; 2000US-0250391.	PR
PR		05-DEC-2000; 2000US-0251030.	PR
PR		05-DEC-2000; 2000US-0251988.	PR
PR		05-DEC-2000; 2000US-0256719.	PR
PR		06-DEC-2000; 2000US-0251479.	PR
PR		06-DEC-2000; 2000US-0251856.	PR
PR		08-DEC-2000; 2000US-0251868.	PR
PR		08-DEC-2000; 2000US-0253063.	PR
PR		08-DEC-2000; 2000US-0253064.	PR
PR		08-DEC-2000; 2000US-0253065.	PR
PR		08-DEC-2000; 2000US-0253190.	PR
PR		11-DEC-2000; 2000US-0254097.	PR


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PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis
XX
XX Disclosure; SEQ ID NO 25259; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 27082 BP; 5963 A; 7786 C; 7711 G; 5622 T; 0 other;

Query Match 13.8%; Score 32.2; DB 22; Length 27082;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Oy 14 TGCCCTGTGCTCTTGTACCCCTTGGCAGCTCACATGGACAGCGCGGTATGA 73
Db 13061 TGTCCCTGACCCCTACTCTTCTGGGGACTTCTAGCCACAGCGGTGGCTGG 13120

Oy 74 CTTTCAACTCAAGCTG 90
Db 13121 ACTTCAACTCAGGTG 13137

RESULT 15
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ID AAL05122 standard; DNA; 13216 BP.
AC AAL05122;
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XX 21-NOV-2001 (first entry)
XX
XX Human reproductive system related antigen DNA SEQ ID NO: 7810.
XX
XX Human; reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy; ds.
XX
XX Homo sapiens.
XX
XX WO200155320-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01339.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
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PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 180 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;
US-09-092-296-3
;
Query Match          100.0%; Score 180; DB 9; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.9e-54;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCTCTCTTGGACCCCTCT 60
    |||||||
Db 1 CAGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCTCTCTTGGACCCCTCT 60
    |||||||

QY 61 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
    |||||||
Db 61 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
    |||||||

QY 121 TCTGACAAGTCTCTCTATGAGTCCAGCTTCTTGAATTCGTTGAAAAGCTCTGCCTCT 180
    |||||||
Db 121 TCTGACAAGTCTCTCTATGAGTCCAGCTTCTTGAATTCGTTGAAAAGCTCTGCCTCT 180
    |||||||

RESULT 2
US-09-092-296-5
; Sequence 5, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
;   FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 389 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
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US-09-092-296-5
;
Query Match          100.0%; Score 180; DB 9; Length 389;
Best Local Similarity 100.0%; Pred. No. 7.7e-54;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCTCTCTTGGACCCCTCT 60
    |||||||
Db 1 CAGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCTCTCTTGGACCCCTCT 60
    |||||||

QY 61 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
    |||||||
Db 61 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
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QY 121 TCTGACAAGTCTCTCTATGAGTCCAGCTTCTTGAATTCGTTGAAAAGCTCTGCCTCT 180
    |||||||
Db 121 TCTGACAAGTCTCTCTATGAGTCCAGCTTCTTGAATTCGTTGAAAAGCTCTGCCTCT 180
    |||||||

RESULT 3
US-09-092-296-6
; Sequence 6, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
;   FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 413 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;
US-09-092-296-6
;
Query Match          99.1%; Score 178.4; DB 9; Length 413;
Best Local Similarity 99.4%; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/089948
 ; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/089952
 ; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/090246
 ; PRIOR FILING DATE: 1998-06-22
 ; PRIOR APPLICATION NUMBER: 60/090252
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 ; PRIOR FILING DATE: 1998-07-09
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 99.18; Score 178.4; DB 9; Length 422;
 Best Local Similarity 99.48; Pred. No. 2.9e-53;
 Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGAGCGCAGTGGCCACTATGGGTCTGGGCTGCCCTTGTCTCTCTTGACCCCTCT 60
 DB 39 CAGGAGCGCAGTGGCCACTATGGGTCTGGGCTGCCCTTGTCTCTCTTGACCCCTCT 98
 QY 61 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
 DB 99 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158
 QY 121 TCTGACAAGTTCCTCTCTATGAGTCCAGCTTCTCTGGAATTGCTTGAAGAGCTCTGCCTCTCT 180
 DB 159 TCTGACAAGTTCCTCTCTATGAGTCCAGCTTCTCTGGAATTGCTTGAAGAGCTCTGCCTCTCT 218

RESULT 5
 US-09-989-293A-362
 ; Sequence 362, Application US/09989293A
 ; Patent No. US2002017164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC66
 ; CURRENT APPLICATION NUMBER: US/09/989,293A
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
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 ; PRIOR FILING DATE: 1998-02-25
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 ; PRIOR APPLICATION NUMBER: 60/083322
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 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/087106
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 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/087609
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/087759


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Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGGAGCGAGTGGCCACTATGGGTCTGGGCTGCCCTTGCTCCTCTTGACCCCTCCT 60
Db 39 CAGGAGCGAGTGGCCACTATGGGTCTGGGCTGCCCTTGCTCCTCTTGACCCCTCCT 98
QY 61 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 99 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158
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RESULT 6
US-10-063-547-65
; Sequence 65, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P323ORIC1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-547-65

Query Match 99.1%; Score 178.4; DB 9; Length 422;
Best Local Similarity 99.4%; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGGAGCGAGTGGCCACTATGGGTCTGGGCTGCCCTTGCTCCTCTTGACCCCTCCT 60
Db 39 CAGGAGCGAGTGGCCACTATGGGTCTGGGCTGCCCTTGCTCCTCTTGACCCCTCCT 98
QY 61 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 99 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158
QY 121 TCTGACAAGTCTCCTCATGAGTCCAGCTTCTGGAATTCCTTGAAGAGCTCTGCCCTCCT 180
Db 159 TCTGACAATTCCTCCTCATGAGTCCAGCTTCTGGAATTCCTTGAAGAGCTCTGCCCTCCT 218

RESULT 7
US-09-989-735-362
; Sequence 362, Application US/09989735
; Publication No. US2002019329A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

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Query Match 99.1%; Score 178.4; DB 9; Length 422;

Best Local Similarity 99.4%; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCTCTCTTGACCCCTCT 60
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Db 39 CAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCTCTCTTGACCCCTCT 98
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QY 61 TGGCAGCTCACATGGAACAGAGCGGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
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RESULT 10

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US-09-950-436-362
; Sequence 362, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

```

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William J.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: P2730P1C14
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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; PRIOR FILING DATE: 1998-07-09

Query Match 99.18; Score 178.4; DB 9; Length 422;
Best Local Similarity 99.48; Pred No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGAGCGCAGTGGCCACTATGCGGTCTGGGCTGCCCTTGCTCTCTTGAACCTCCT 60
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QY 61 TGGCAGCTCATATGGAACAGCGCGGTATGACTTTGCAACTGAAGTGAAGGAGTCTTT 120
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QY 121 TCTGCAAGTCTCTCTATGAGTCCAGCTTCTCGAATGCTGAAAAGCTCGCTCCT 180
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RESULT 11
US-09-991-181-362
; Sequence 362, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
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; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
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; PRIOR FILING DATE: 1998-06-05
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; PRIOR APPLICATION NUMBER: 60/088655
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-07-09
;
Query Match 99.1%; Score 178.4; DB 9; Length 422;
Best Local Similarity 99.4%; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAGGAGCGCAGTGGCCACTATGGGCTGTGGGCTGCCCCCTTGTCTCTCTTGACCTCCT 60
Db 39 CAGGAGCGCAGTGGCCACTATGGGCTGTGGGCTGCCCCCTTGTCTCTCTTGACCTCCT 98
Qy 61 TGGCAGCTCATGTGAACAGGCGCGGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 99 TGGCAGCTCATGTGAACAGGCGCGGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158
Qy 121 TCTGACAAAGTTCTCTCTATGATGAGTCCAGCTTCCCTGGAATTTGTTGAAAGCTCTGCCTCCT 180
Db 159 TCTGACAAAGTTCTCTCTATGATGAGTCCAGCTTCCCTGGAATTTGTTGAAAGCTCTGCCTCCT 218

RESULT 12
US-09-993-687-362
; Sequence 362, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC11
CURRENT APPLICATION NUMBER: US/09/993,687
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444

[illegible]

RESULT 14
US-09-997-653-362
; Sequence 362, Application US/09997653
; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashtenazi, Avi J.
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match          99.1%; Score 178.4; DB 9; Length 422;
Best Local Similarity 99.4%; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CAGAGCGCAGTGGCCACTATGGGCTGGGCTGCCCTTGTCTCTCTCTTGACCCCTCT 60
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Db 39 CAGAGCGCAGTGGCCACTATGGGCTGGGCTGCCCTTGTCTCTCTCTTGACCCCTCT 98

QY 61 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
   |||||
Db 99 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158

QY 121 TCTGACAAGTTCCTCTATGAGTCCAGCTTCTCTGGAATTGCTTGAAGAAGCTCTGCCTCT 180
   |||||
Db 159 TCTGACAATTCCTCTATGAGTCCAGCTTCTCTGGAATTGCTTGAAGAAGCTCTGCCTCT 218
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RESULT 15
US-10-174-590-241
; Sequence 241, Application US/10174590
; Publication No. US2003008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
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; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Fan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; PRIOR application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-241
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Query Match          99.1%; Score 178.4; DB 9; Length 422;
Best Local Similarity 99.4%; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 CAGAGCGCAGTGGCCACTATGGGCTGGGCTGCCCTTGTCTCTCTCTTGACCCCTCT 60
   |||||
Db 39 CAGAGCGCAGTGGCCACTATGGGCTGGGCTGCCCTTGTCTCTCTCTTGACCCCTCT 98

QY 61 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
   |||||
Db 99 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158

QY 121 TCTGACAAGTTCCTCTATGAGTCCAGCTTCTCTGGAATTGCTTGAAGAAGCTCTGCCTCT 180
   |||||
Db 159 TCTGACAATTCCTCTATGAGTCCAGCTTCTCTGGAATTGCTTGAAGAAGCTCTGCCTCT 218
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Job time : 50.3673 secs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 580 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 91..480
US-08-627-610-7

Query Match 16.9%; Score 30.4; DB 2; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.3;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 8 GCAGTGGCCACTATGGGTCTGGGCTGCGCCCTTGTCTCTTGACCTCTTGGCAGC 67
Db 128 GCGGTGGCCAGGCGCGCTGCTGCTGCGCCCAACATGCGCTGTGCCCGTCTGTGGC 69
QY 68 TCACATGGACAGGCGCGGTATGACTTTGCAACTG 103
Db 68 AGAAATGGCTTCGCGCGCGGTGAGATTGCTACAG 33

RESULT 3
US-08-581-918A-7/c
; Sequence 7, Application US/08581918A
; Patent No. 6043030
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 580 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 91..480
US-08-581-918A-7
Query Match 16.9%; Score 30.4; DB 3; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.3;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 8 GCAGTGGCCACTATGGGTCTGGGCTGCGCCCTTGTCTCTTGACCTCTTGGCAGC 67
Db 128 GCGGTGGCCAGGCGCGCTGCTGCTGCGCCCAACATGCGCTGTGCCCGTCTGTGGC 69
QY 68 TCACATGGACAGGCGCGGTATGACTTTGCAACTG 103
Db 68 AGAAATGGCTTCGCGCGCGGTGAGATTGCTACAG 33

RESULT 4
US-08-346-147B-7/c
; Sequence 7, Application US/08346147B
; Patent No. 6211334
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: WordPad
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/346,147B
;; FILING DATE: 29-NOV-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/306,511
;; FILING DATE: 14-SEP-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/248,812
;; FILING DATE: 25-MAY-1994
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 08/227,371
;; FILING DATE: 14-APR-1994
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 08/154,915
;; FILING DATE: 18-NOV-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/991,997
;; FILING DATE: 17-DEC-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Vincent, Matthew P.
;; REGISTRATION NUMBER: 36,709
;; REFERENCE/DOCKET NUMBER: MIV-071.04
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 832-1299
;; TELEFAX: (617) 832-7000
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 580 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 91...480
US-08-346-147B-7

Query Match 16.9%; Score 30.4; DB 4; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.3;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 8 GCAGTGGCCACTATATGGGTCTGGGCTGCCCTTGTCTCTCTTGTGACCTCTCTTGGCAGC 67
Db 128 GCGGTGGCCAGCGCCGCTCACTGCTGCGGCCCAACATGCCCTGTGCCCGGTCTGTGGC 69
QY 68 TCACATGGAACAGCGCGGGGTATGACTTTGCAACTG 103
Db 68 AGAAATGGTCTTCGCCGCGGTGAGATTGCTACAG 33

RESULT 5
US-08-822-936-7/c
; Sequence 7, Application US/08822936
; Patent No. 6242575
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koff, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Isolated p27 Protein, Nucleic Acid
; TITLE OF INVENTION: Molecules Encoding Same, Methods of Identifying Agents Acting
; TITLE OF INVENTION: and Uses of Said Agents
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot, LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/822,936
;; FILING DATE: 21-FEBRUARY-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Vincent, Matthew P.
;; REGISTRATION NUMBER: 36,709
;; REFERENCE/DOCKET NUMBER: MIV-079.05
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 832-1000
;; TELEFAX: (617) 832-7000
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 580 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 91...480
US-08-822-936-7

Query Match 16.9%; Score 30.4; DB 4; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.3;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 8 GCAGTGGCCACTATATGGGTCTGGGCTGCCCTTGTCTCTCTTGTGACCTCTCTTGGCAGC 67
Db 128 GCGGTGGCCAGCGCCGCTCACTGCTGCGGCCCAACATGCCCTGTGCCCGGTCTGTGGC 69
QY 68 TCACATGGAACAGCGCGGGGTATGACTTTGCAACTG 103
Db 68 AGAAATGGTCTTCGCCGCGGTGAGATTGCTACAG 33

RESULT 6
US-08-497-214D-7/c
; Sequence 7, Application US/08497214D
; Patent No. 6331390
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,214D
; FILING DATE: 30-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..480
; US-08-497-214D-7

Query Match 16.9%; Score 30.4; DB 4; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.3;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 8 GCAGTGGCCACTATGGGCTGCGGCTGCTCCCTCTGTGACCTCTTGGCAGC 67
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Db 128 GCGGTGCCAGGCCGCGTCACTGCTGCCGCCAACATGCCCTGTGCCCGTCTGTGGC 69

QY 68 TCACATGGACAGGCCGGTATGACTTGCACATG 103
   || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 68 AGAAATGGTCTTCGCCGCGGTGAGATTGCTACAG 33

RESULT 7
PCT-US95-04636-7/c
; Sequence 7, Application PC/TUS9504636
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04636
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..480
; PCT-US95-04636-7

Query Match 16.9%; Score 30.4; DB 5; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.3;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 8 GCAGTGGCCACTATGGGCTGCGGCTGCTCCCTCTGTGACCTCTTGGCAGC 67
   || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 128 GCGGTGCCAGGCCGCGTCACTGCTGCCGCCAACATGCCCTGTGCCCGTCTGTGGC 69

QY 68 TCACATGGACAGGCCGGTATGACTTGCACATG 103
   || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 68 AGAAATGGTCTTCGCCGCGGTGAGATTGCTACAG 33

RESULT 8
US-09-219-194-2
; Sequence 2, Application US/09219194
; Patent No. 6410230
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; TITLE OF INVENTION: GLYCERALDEHYDE-3-PHOSPHATE
; DEHYDROGENASE AND NUCLEAR RESTORATION OF CYTOPLASMIC MAL
; STERILITY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: SWABEY OGILVY RENAULT
; STREET: 1961 McGill College Ave. - Suite 1600
; CITY: Montreal
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/219,194
; FILING DATE: 23-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/020,553
; FILING DATE: 26-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cote, France
; REGISTRATION NUMBER: 4166
; REFERENCE/DOCKET NUMBER: 1770-152"PCT" FC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 514 845-7126
; TELEFAX: 514-288-8389
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-219-194-2

Query Match 16.9%; Score 30.4; DB 4; Length 1091;
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Best Local Similarity 63.9%; Pred. No. 0.39; Mismatches 26; Indels 0; Gaps 0;
Matches 46; Conservative 0;

Qy 58 CCTTGGAGCTCAGTGGACAGCGCGGGTATGACTTTGCACTGGAAGTGAAGGATC 117
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Db 263 CTGAGGATATCCCATGGGGTGGAGCGGAGCTGACTTTGTTGATGCTACTGGTGC 322
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Qy 118 TTTTCTGACAAG 129
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Db 323 TTAGCTGACAAG 334

RESULT 9
US-08-928-383B-25
; Sequence 25, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Cocksackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1515 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1095
US-08-928-383B-25

Query Match 16.9%; Score 30.4; DB 4; Length 1515;
Best Local Similarity 61.2%; Pred. No. 0.45; Mismatches 0; Indels 0; Gaps 0;
Matches 49; Conservative 0;

Qy 2 AGGAGCGCAGTGGCAGTATGGGCTGGGCTGGCCCTTGTCTCTCTCTTGTACCCCTCTT 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 712 ACGATCGGGCGCGCTATAGGAGCGTGTGCGCCCTTGTGCTCATCGGGGCATCCCTC 771
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 62 GGCAGCTCACATGGAACAGG 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 772 TTCTGCTGTACAGGAACG 791

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```

RESULT 10
US-09-221-017B-850
; Sequence 850, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P11182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P29111
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 850:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2870 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORYPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1...2870
US-09-221-017B-850

Query Match 16.3%; Score 29.4; DB 4; Length 2870;
Best Local Similarity 56.8%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;
Matches 54; Conservative 0;

Qy 64 CAGCTCACATGGAACAGGCGCGGCTATGACTTTGCACTGGAAGTGAAGTCTTTTCT 123
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Db 2673 CAGCTCATAGTCAACGTCGATTTGAGACGTCAGCCTTTGAAGGGTTCCGCGTTTGGG 2732
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Qy 124 GACAGTTCTCTTATGAGTCCAGCTTCTCGAAT 158
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Db 2733 GGTGAGCTCCACCTGTGTTTCCCGAGATGCCCGAAT 2767

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 03:08:45 ; Search time 901.429 Seconds
(without alignments)
3233.964 Million cell updates/sec

Title: US-09-092-296-3
Perfect score: 180
Sequence: 1 CAGGAGCGCAGTGGCCACTA.....CTTGAAGAGCTGCGCTCCT 180

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estma:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fut:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_oth:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
c 1	180	100.0	449	10	AW293443
c 2	178.4	99.1	456	12	BC506690
c 3	176.8	98.2	830	13	BI759796
c 4	166.4	92.4	422	12	BF002050
c 5	119.6	66.4	895	13	BI820029
c 6	106.6	59.2	865	13	BI820110

c 7	100.4	55.8	404	9	AI857998
c 8	85.8	47.7	361	12	BF521842
c 9	83	46.1	521	10	BS533837
c 10	83	46.1	522	10	BS533837
c 11	74.2	41.2	552	17	AQ18761
c 12	55.6	30.9	328	9	AI136523
c 13	44.4	24.7	506	17	AZ241329
c 14	44.4	24.7	633	17	AZ079350
c 15	36.2	20.1	261	10	BB411111
c 16	33.4	18.6	568	17	AQ290553
c 17	33.2	18.4	533	13	BM317927
c 18	32.4	18.0	709	10	BS355728
c 19	32.4	18.0	434	13	BI186111
c 20	32.4	18.0	523	10	AW128453
c 21	32.4	18.0	537	10	AW078074
c 22	32.4	18.0	562	13	BI683276
c 23	32.4	18.0	582	13	BI706799
c 24	32.4	18.0	2252	17	BH770934
c 25	31.8	17.7	408	10	AW405843
c 26	31.6	17.6	1143	12	BE871161
c 27	31.6	17.6	343	10	BS446166
c 28	31.6	17.6	468	14	BQ743962
c 29	31.6	17.6	550	12	BF779666
c 30	31.6	17.6	919	14	BQ228365
c 31	31.4	17.4	339	14	F08745
c 32	31.4	17.4	623	10	BS616110
c 33	31.2	17.3	669	17	AG037872
c 34	31.2	17.3	777	13	BI911281
c 35	31.2	17.3	1031	14	BQ960402
c 36	31	17.2	376	13	BM401493
c 37	31	17.2	389	13	BM401452
c 38	31	17.2	396	10	AV525985
c 39	31	17.2	431	13	BM401638
c 40	31	17.2	440	13	BM401560
c 41	31	17.2	472	13	BM401478
c 42	31	17.2	516	13	BM401409
c 43	31	17.2	538	10	BS769028
c 44	31	17.2	545	14	T41524
c 45	31	17.2	548	13	BM401534

ALIGNMENTS

RESULT 1
AW293443/c
LOCUS AW293443 449 bp mRNA linear EST 16-JAN-2000
DEFINITION UI-H-B12-ahm-c-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2727182 3', mRNA sequence.
ACCESSION AW293443
VERSION AW293443.1 GI:6700079
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 449)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA-yes. Location/Qualifiers

AI857998 w169b01.x
BS521842 UI-R-C2p-
BS533837 BS533837
BS664284 BS664284
AQ18761 HS_5511_B
AI136523 UI-R-C2p-
AZ241329 RPCI-23-7
AZ079350 RPCI-23-4
BB411111 BB411111
AQ290553 bxb0037C
BM317927 FL1_13_CO
BS355728 DGL116.G
BI186111 fp73b11.y
AW128453 fe16b05.y
AW078074 fe24b05.y
BI683276 464604.MA
BI706799 fq10e03.y
BH770934 LMGtag66
AW405843 UI-HF-B10
BE871161 601448727
BS446166 BS446166
BQ743962 WHE4110.B
BF779666 3232-2.h1
BQ228365 AGENCOURT
F08745 HSC1DB011.n
BS616110 BS616110
AG037872 pan trogl
BI911281 603062883
BQ960402 AGENCOURT
BM401493 JH2B05F.S
BM401452 JH1B11F.S
AV525985 AV525985
BM401638 JL1G12F.S
BM401560 JH3G08F.S
BM401478 JH1G05F.S
BM401409 GH038F.Sn
BS769028 BS769028
T41524 10105.Lambd
BM401534 JH3A12F.S

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM11444 row: m column: 20
 High quality sequence stop: 432.

FEATURES

source
 1. .830
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5186107"
 /clone_lib="NIH_MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
 BASE COUNT 175 a 276 c 210 g 168 t 1 others
 ORIGIN

Query Match 98.2%; Score 176.8; DB 13; Length 830;
 Best Local Similarity 98.9%; Pred. No. 4.4e-42;
 Matches 178; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAGGAGCGAGTGGGCTATGGGCTGCGGCTGCTGCTCTCTGACCCCTCT 60
 Db 62 CAGGAGCGAGTGGGCTATGGGCTGCGGCTGCTGCTCTCTGACCCCTCT 121
 QY 61 TGCAGCTCACATGGAACAGCGCGGGTATGCTTGCACCTGAAGGAGTCTTT 120
 Db 122 TGCAGCTCACATGGAACAGCGCGGGTATGCTTGCACCTGAAGGAGTCTTT 181
 QY 121 TCTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTCCTGAAAGCTCTGCCCTCT 180
 Db 182 TCTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTCCTGAAAGCTCTGCCCTCT 241

RESULT 4
 BF002050/c
 LOCUS 7998c11.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:3314516 3',
 DEFINITION mRNA sequence.
 ACCESSION BF002050
 VERSION BF002050.1 GI:10702325
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 422)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov

Seq primer: -40UP from Gibco.
 Location/Qualifiers
 1. .422
 source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3314516"
 /clone_lib="NCI_CGAP_Col6"
 /tissue_type="colon tumor, RER+"
 /lab_host="DH10B"
 /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site: 1: NotI; Site: 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Col0 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 1057416-1061255, and 1144584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 102 a 99 c 130 g 88 t 3 others
 ORIGIN
 Query Match 92.4%; Score 166.4; DB 12; Length 422;
 Best Local Similarity 99.4%; Pred. No. 4.1e-39;
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGGAGCGAGTGGGCTATGGGCTGCGGCTGCTGCTCTCTGACCCCTCT 60
 Db 396 CAGGAGCGAGTGGGCTATGGGCTGCGGCTGCTGCTCTCTGACCCCTCT 337
 QY 61 TGCAGCTCACATGGAACAGCGCGGGTATGCTTGCACCTGAAGGAGTCTTT 120
 Db 336 TGCAGCTCACATGGAACAGCGCGGGTATGCTTGCACCTGAAGGAGTCTTT 277
 QY 121 TCTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTCCTTGAAGG 168
 Db 276 TCTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTCCTTGAAGG 229

RESULT 5
 B1820029
 LOCUS 603037210F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178171 5',
 DEFINITION mRNA sequence.
 ACCESSION B1820029
 VERSION B1820029.1 GI:15931579
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 895)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM11444 row: c column: 04
 High quality sequence start: 5
 High quality sequence stop: 422.
 Location/Qualifiers
 1. .895
 source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5178171"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"

Query Match 55.8%; Score 100.4; DB 9; Length 404;
 Best Local Similarity 98.1%; Pred. No. 1.9e-19;
 Matches 101; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 78 CAGGCGGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAAGTTCCTCT 137
 DB 311 CAGGCGGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCT 252
 QY 138 ATGAGTCCAGCTTCCTCGAATTGCTTGAAGAAGCTCTGCCTCT 180
 DB 251 ATGAGTCCAGCTTCCTCGAATTGCTTGAAGAAGTCTGCCTCT 209

RESULT 8
 BF521842 361 bp mRNA linear EST 11-DEC-2000
 LOCUS UI-R-C2p-ng-e-02-0-UI.r1 UI-R-C2p Rattus norvegicus cDNA clone
 DEFINITION UI-R-C2p-ng-e-02-0-UI 5', mRNA sequence.
 ACCESSION BF521842
 VERSION BF521842.1 GI:11629809
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 361)
 REFERENCE Ronald M.F., Lennon, G. and Soares, M.B.
 AUTHORS Normalization and subtraction: two approaches to facilitate gene
 TITLE discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: mscares@blue.weeg.uiowa.edu
 cDNA library preparation: M.B. Soares Lab Clone distribution:
 clones will be available through Research Genetics (www.resgen.com)
 This clone is also available through the I.M.A.G.E. Consortium at
 LLNL (info@image.llnl.gov). IMAGE ID= 1792770
 Seq primer: M13 Forward.

FEATURES
 Location/Qualifiers
 1..361
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-C2p-ng-e-02-0-UI"
 /clone_lib="UI-R-C2p"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-pac (Pharmacia)"
 polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
 library is a subtracted library derived from the UI-R-C1
 library, which is a subtracted library derived from the
 UI-R-C0 library. The UI-R-C0 library consisted of a
 mixture of individually tagged normalized libraries
 constructed from rat placenta, adult lung, brain, liver,
 kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
 embryo. The tag is a string of 3-5 nucleotides present
 between the Not I site and the oligo-dr track which allows
 identification of the library of origin of a clone within
 the mixture. The subtracted library (UI-R-C2p) was
 constructed as follows: PCR amplified cDNA inserts from
 UI-R-C1 clones from which 3' ESTs had been derived was
 used as a driver in a hybridization with the UI-R-C1
 library in the form of single-stranded circles. The
 remaining single-stranded circles (subtracted library) was
 purified by hydroxyapatite column chromatography,
 converted to double-stranded circles and electroporated

into DH10B bacteria (Life Technologies) to generate the
 UI-R-C2p library. This procedure has been previously
 described (Bonaldo, Lennon and Soares, Genome Research 6:
 791-806, 1996)*

BASE COUNT 79 a 121 c 91 g 70 t

Query Match 47.7%; Score 85.8; DB 12; Length 361;
 Best Local Similarity 67.8%; Pred. No. 4.1e-15;
 Matches 120; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 4 GAGCCAGTGGCCACATATGGGTCTGGGCTGCCCCCTGTCCTCTGACCTCTGG 63
 DB 6 GGGTGAAGCGGCCACCATGGAGCCTTCGATGTGCTCTTCCTCTGACCTCTG 65
 QY 64 CAGCTCACATGGAACAGCGCCGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCT 123
 DB 66 CAGCTCACTGAAGGCCCAACAAGGTGACTTTGCAAGTAAACTGACCGGCATCTCA 125
 QY 124 GACAAGTTCCTCTCTATGAGTCCAGCTTCCTCGAATTGCTTGAAGTCTGCTCTCT 180
 DB 126 GGCCAAGACCTCCCAAGACTCGGCTTCTGGACATGCTCCAAAAGATCTGCTCTCT 182

RESULT 9
 BB533837 521 bp mRNA linear EST 26-OCT-2001
 LOCUS BB533837 RIKEN full-length enriched, 0 day neonate lung Mus
 DEFINITION musculus cDNA clone E030032D13 3', mRNA sequence.

ACCESSION BB533837
 VERSION BB533837.2 GI:16446306
 KEYWORDS EST.
 SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
 Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
 M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
 Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
 D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
 Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
 Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 Unpublished (2001)

TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

JOURNAL

COMMENT On Jul 29, 2000 this sequence version replaced gi:9585766.

Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura

S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara

,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES
Source
1. .521
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="E030032D13"
/clone_lib="RIKEN full-length enriched, 0 day neonate lung"
/tissue_type="lung"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/notes="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGCGCGCACTGCAGTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGATTCGAGTTAAATTAATTAATTCGCCGCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT 119 a 163 c 125 g 114 t
ORIGIN

Query Match 46.1%; Score 83; DB 10; Length 521;
Best Local Similarity 70.4%; Pred. No. 3.4e-14;
Matches 126; Conservative 0; Mismatches 50; Indels 3; Gaps 1;
QY 2 AGAGCGCAGTGGCCATATGGGTCTGGGTGCGCCCTTCTCTCTCTTGACCCCTCTT 61
DB 156 AGCGTGGGTAGCCACCATTGAGTCTTTGATGCGCTCTTCTCTCTCTGCGCCCTC 215
QY 62 GCGAGTCTACATGNAAGCGCGGTATGACTTTGCACTGAAGCTGAAGAGTCTTTT 121
DB 216 AGCAGCTCACG---CAGGCGCCAAAGGTGACTTTGCAGTAAAGCTGACCGAGACTTT 272
QY 122 CTGACAAGTTCTCTATGAGTCCAGCTTCTCTGGAATTCGTTGAAAGCTCTGCTCCT 180
DB 273 CAGGACAAGACCTCCCAAGACTCCAGTGTCTGGACATGCTCCAAAAGATCTGCTCCT 331

RESULT 10
BB664284
LOCUS
DEFINITION
musculus cDNA clone E030032D13 5', mRNA sequence.
BB664284.1 GI:16498038
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 522)
AUTHORS
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,

TITLE
JOURNAL
COMMENT

Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp
URL:<http://genome.gsc.riken.go.jp/>
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsumura ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara ,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
e mouse tissues.
Location/Qualifiers
1. .522
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="E030032D13"
/clone_lib="RIKEN full-length enriched, 0 day neonate lung"
/tissue_type="lung"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/notes="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGCGCGCACTGCAGTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGATTCGAGTTAAATTAATTAATTAATTCGCCGCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

FEATURES
Source

BASE COUNT 132 a 151 c 125 g 114 t
ORIGIN
Query Match 46.1%; Score 83; DB 10; Length 522;
Best Local Similarity 70.4%; Pred. No. 3.4e-14;
Matches 126; Conservative 0; Mismatches 50; Indels 3; Gaps 1;
QY 2 AGAGCGCAGTGGCCATATGGGTCTGGGTGCGCCCTTCTCTCTCTTGACCCCTCTT 61

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:55:40 ; Search time 123.673 Seconds
(without alignments)
3277.661 Million cell updates/sec

Title: US-09-092-296-3
Perfect score: 180
Sequence: 1 CAGGAGCGCAGTGGCCACTA.....CTTGAAAGCTCTGCTCTCT 180

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Result No.	Query Match	Score	Length	ID	Description
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2	178.4	99.1	422	22	AAZ65087
3	178.4	99.1	422	22	AAZ65087
4	178.4	99.1	422	22	AAZ65087
5	178.4	99.1	422	22	AAZ65087
6	178.4	99.1	422	22	AAZ65087
7	178.4	99.1	422	22	AAZ65087
8	178.4	99.1	422	22	AAZ65087
9	178.4	99.1	422	22	AAZ65087
10	178.4	99.1	422	22	AAZ65087
11	178.4	99.1	422	22	AAZ65087
12	178.4	99.1	422	22	AAZ65087
13	178.4	99.1	422	22	AAZ65087
14	178.4	99.1	422	22	AAZ65087
15	178.4	99.1	422	22	AAZ65087
16	178.4	99.1	422	22	AAZ65087
17	178.4	99.1	422	22	AAZ65087
18	178.4	99.1	422	22	AAZ65087
19	178.4	99.1	422	22	AAZ65087
20	178.4	99.1	422	22	AAZ65087
21	178.4	99.1	422	22	AAZ65087
22	178.4	99.1	422	22	AAZ65087
23	178.4	99.1	422	22	AAZ65087
24	178.4	99.1	422	22	AAZ65087
25	178.4	99.1	422	22	AAZ65087
26	178.4	99.1	422	22	AAZ65087
27	178.4	99.1	422	22	AAZ65087
28	178.4	99.1	422	22	AAZ65087
29	178.4	99.1	422	22	AAZ65087
30	178.4	99.1	422	22	AAZ65087
31	178.4	99.1	422	22	AAZ65087
32	178.4	99.1	422	22	AAZ65087
33	178.4	99.1	422	22	AAZ65087
34	178.4	99.1	422	22	AAZ65087
35	178.4	99.1	422	22	AAZ65087
36	178.4	99.1	422	22	AAZ65087
37	178.4	99.1	422	22	AAZ65087
38	178.4	99.1	422	22	AAZ65087
39	178.4	99.1	422	22	AAZ65087
40	178.4	99.1	422	22	AAZ65087
41	178.4	99.1	422	22	AAZ65087
42	178.4	99.1	422	22	AAZ65087
43	178.4	99.1	422	22	AAZ65087
44	178.4	99.1	422	22	AAZ65087
45	178.4	99.1	422	22	AAZ65087

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	32.2	17.9	27082	22	AAK70447	Human immune/haema
11	32	17.8	1128	19	AAV28846	Mouse coxsackievir
12	31.6	17.6	550	21	AAK93727	Cat flea hindgut a
13	31.2	17.3	16596	22	AAK83767	Human immune/haema
14	31.2	17.3	16596	22	AAK83767	Human immune/haema
15	30.8	17.1	11749	22	AAK36066	DNA encoding human
16	30.8	17.1	11749	22	AAK36066	Human musculoskele
17	30.8	17.1	11749	22	AAK40590	DNA encoding human
18	30.8	17.1	11749	22	AAK40590	Human reproductive
19	30.8	17.1	11749	22	AAK64782	Human immune/haema
20	30.8	17.1	30420	22	AAK36067	Human musculoskele
21	30.8	17.1	30420	22	AAK36067	DNA encoding human
22	30.4	16.9	580	16	AAK06476	Human reproductive
23	30.4	16.9	580	16	AAK06476	Cell-cycle regulat
24	30.4	16.9	580	20	AAK80475	Mouse INK-4 protei
25	30.4	16.9	580	21	AAK13099	Murine cell cycle
26	30.4	16.9	580	24	ABK13272	Mouse cDNA encodin
27	30	16.7	665	21	AAV50430	Mouse coxsackievir
28	30	16.7	820	24	ABN36996	Arabidopsis thalia
29	30	16.7	831	21	AAK51574	Arabidopsis thalia
30	30	16.7	833	21	AAK37811	Arabidopsis thalia
31	30	16.7	843	21	AAK51564	Arabidopsis thalia
32	30	16.7	845	21	AAK35459	Arabidopsis thalia
33	30	16.7	879	21	AAK52193	Arabidopsis thalia
34	29.8	16.6	291	20	AAK86365	EST clone AR34. H
35	29.8	16.6	1695	22	AAK14885	Human cDNA encodin
36	29.8	16.6	1788	22	AAK26848	Human cDNA encodin
37	29.6	16.4	10388	22	AAI98966	Human excretory re
38	29.6	16.4	10388	22	AAI63316	Human kidney relat
39	29.6	16.4	11294	23	ABL04652	Drosophila melanog
40	29.4	16.3	1251	24	ABK09969	Eastern cottonmout
41	29.4	16.3	7275	23	ABL04215	Drosophila melanog
42	29.4	16.3	12235	23	ABL04214	Drosophila melanog
43	29.2	16.2	1359	23	AAK71696	DNA encoding novel
44	29	16.1	977	23	ABK42212	Genomic sequence #
45	29	16.1	4417	21	AAA47479	Murine TANGO 197 c

ALIGNMENTS

RESULT 1
AAZ65087
ID AAZ65087 standard; cDNA; 422 BP.
XX AAZ65087;
AC AAZ65087;
DT 05-APR-2000 (first entry)
XX Membrane-bound protein PRO1098 encoding cDNA.

XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
XX pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX Homo sapiens.
XX WO963088-A2.
XX 09-DEC-1999.
XX 02-JUN-1999; 99WO-0512252.
XX 02-JUN-1998; 98US-0087607.
XX 02-JUN-1998; 98US-0087609.
XX 02-JUN-1998; 98US-0087759.
XX 03-JUN-1998; 98US-0087827.
XX 04-JUN-1998; 98US-0088021.
XX 04-JUN-1998; 98US-0088025.
XX 04-JUN-1998; 98US-0088028.
XX 04-JUN-1998; 98US-0088029.
XX 04-JUN-1998; 98US-0088030.
XX 04-JUN-1998; 98US-0088033.
XX 04-JUN-1998; 98US-0088326.

PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090451.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091344.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.

PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096729.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.

(GETH) GENENTECH INC.

BAker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;

WPI; 2000-072883/06.
P-PSDB; AAY66741.

Membrane-bound proteins and related nucleotide sequences -

Claim 2; Fig 257; 822pp; English.

CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be

employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.

Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 99.1%; Score 178.4; DB 21; Length 422;
Best Local Similarity 99.4%;
Pred. No. 1.9e-49;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	CAGGACGGCAGTGGCCACTATGCGGTCTGGCTGCCCTCTGTCTCTCTTGACCCTCT	60
Db	39	CAGGACGGCAGTGGCCACTATGCGGTCTGGCTGCCCTCTGTCTCTCTTGACCCTCT	98
QY	61	TGCAGCTCACATGGACAGCGCCGGTATGACTTTGCACTGAAGCTGAAGGAGTCCTTT	120
Db	99	TGCAGCTCACATGGACAGCGCCGGTATGACTTTGCACTGAAGCTGAAGGAGTCCTTT	158
QY	121	TCTGACAAGTTCCTCTATGATGCACAGTCCTCGAATTGCTTGAAGAAGCTCTGCCTCT	180
Db	159	TCTGACAAATTCCTCTATGATGCACAGTCCTCGAATTGCTTGAAGAAGCTCTGCCTCT	218

RESULT 2

AAS46045
ID AAS46045 standard; cDNA; 422 BP.

AC AAS46045:

XX
DT 18-DEC-2001 (first entry)

XX
DE Human DNA encoding PRO polypeptide sequence #121.

PRO polypeptide; mammal; tumour; cancer; human; sheep; ss;
KW
dog; cat; pig; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW
blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW
adrenal; lung; breast; prostate; cervix; liver; genetic disorder;
KW
PCR primer.

OS Homo sapiens.

XX PN WO200168848-A2.

XX
PD 20-SEP-2001.

XX
PF 28-FEB-2001; 2001WO-US06520.

PR	01-MAR-2000;	2000WO-US055601.
PR	02-MAR-2000;	2000WO-US055841.
PR	03-MAR-2000;	2000US-1870200.
PR	05-MAR-2000;	2000US-186968P.
PR	14-MAR-2000;	2000US-189320P.
PR	14-MAR-2000;	2000US-189328P.
PR	15-MAR-2000;	2000WO-US056884.
PR	21-MAR-2000;	2000US-190628P.
PR	21-MAR-2000;	2000US-191007P.
PR	21-MAR-2000;	2000US-191048P.
PR	21-MAR-2000;	2000US-193111P.
PR	28-MAR-2000;	2000US-192655P.
PR	29-MAR-2000;	2000US-193032P.
PR	29-MAR-2000;	2000US-193053P.
PR	30-MAR-2000;	2000WO-US050439.
PR	04-APR-2000;	2000US-194449P.
PR	04-APR-2000;	2000US-194647P.
PR	11-APR-2000;	2000US-195075P.
PR	11-APR-2000;	2000US-196000P.
PR	11-APR-2000;	2000US-196187P.
PR	11-APR-2000;	2000US-196690P.
PR	18-APR-2000;	2000US-196820P.
PR	18-APR-2000;	2000US-198121P.

CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 99.1%; Score 178.4; DB 22; Length 422;
Best Local Similarity 99.4%; Pred. No. 1.9e-49;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGAGCGCAGTGGCCACTATGGGTCTGGCTGGCCCTCTCTCTCTGACCTCTCT 60
DB 39 CAGGAGCGCAGTGGCCACTATGGGTCTGGCTGGCCCTCTCTCTCTGACCTCTCT 98
QY 61 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGTGAAGTCTTT 120
DB 99 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGTGAAGTCTTT 158
QY 121 TCTGACAAATTCCTCTATGAGTCCAGCTTCTCTGGAATTGCTTGAAGCTCTGCTCT 180
DB 159 TCTGACAAATTCCTCTATGAGTCCAGCTTCTCTGGAATTGCTTGAAGCTCTGCTCT 218

RESULT 5
AAZ98124
ID AAZ98124 standard; cDNA: 431 BP.
AC AAZ98124;
XX
DT 11-MAY-2000 (first entry)
XX
DE Human signal peptide containing protein HSP-16 cDNA SEQ ID NO:150.
XX
KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's diseases; ovulatory defect;
KW muscular dystrophy; ss.
XX
OS Homo sapiens.

XX
PN WO200000610-A2.
XX
XX
PD 06-JAN-2000.
XX
XX
PF 25-JUN-1999; 99WO-US14484.
XX
PR 26-JUN-1998; 98US-0090762.
PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX
PA (INCY-) INCYTE PHARM INC.
XX
XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerbloom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
XX
DR WPI; 2000-160673/14.
DR P-PSDB; AAV87239.
XX
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
PS Claim 9; Page 261; 327pp; English.
XX
CC AAZ98109 to AAZ98242 encode AAV87224 to AAV87357 which represent the
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have

CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. HSPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring). In gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. HSP are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSP
CC from natural sources.
XX
SQ Sequence 431 BP; 93 A; 135 C; 101 G; 102 T; 0 other;

Query Match 99.1%; Score 178.4; DB 21; Length 431;
Best Local Similarity 99.4%; Pred. No. 1.9e-49;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGAGCGCAGTGGCCACTATGGGTCTGGCTGGCCCTCTCTCTCTGACCTCTCT 60
DB 32 CAGGAGCGCAGTGGCCACTATGGGTCTGGCTGGCCCTCTCTCTCTGACCTCTCT 91
QY 61 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGTGAAGTCTTT 120
DB 92 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGTGAAGTCTTT 151
QY 121 TCTGACAAATTCCTCTATGAGTCCAGCTTCTCTGGAATTGCTTGAAGCTCTGCTCT 180
DB 152 TCTGACAAATTCCTCTATGAGTCCAGCTTCTCTGGAATTGCTTGAAGCTCTGCTCT 211

RESULT 6
AAV84366
ID AAV84366 standard; cDNA to mRNA; 439 BP.
XX
AC AAV84366;
XX
DT 30-MAR-1999 (first entry)
XX
DE Human stomach carcinoma cDNA clone HP10408.
XX
KW Transmembrane protein; HP10408; human; stomach cancer; ds.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 75..311
FT /*tag= a
FT /note= "cDNA comprising the coding region (minus
FT the stop codon) is claimed (claim 3)"
XX
XX
PN WO9855508-A2.
XX
XX
PD 10-DEC-1998.
XX
XX
PF 03-JUN-1998; 98WO-JP02445.
XX
XX
PR 03-JUN-1997; 97JP-0144948.
XX
XX
PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENTRE.
XX

PI Kato S., Sekine S., Yamaguchi T;
 XX WPI: 1999-045730/04.
 DR P-PSDB; AAW88498.
 XX
 PT New human proteins containing transmembrane domains and their
 PT encoding sequences - useful in the preparation of antibodies and
 PT large-scale protein production, gene diagnosis, and gene therapy
 XX
 PS Claim 4; Page 135; 178pp; English.
 XX
 CC This is the nucleotide sequence of cDNA clone HPI0408, which
 CC includes a coding region (also claimed) for a novel human
 CC transmembrane protein (see AAW88498). The clone was isolated from a
 CC stomach cancer cDNA library using a signal sequence detection
 CC method, and by protein synthesis by in vitro translation. The
 CC encoded protein has a putative signal sequence and a putative
 CC internal transmembrane domain. The invention provides nucleotide
 CC sequences (see AAW84359-76) coding for 18 transmembrane proteins
 CC (see AAW88491-508), vectors containing such polynucleotides, and
 CC eukaryotic cells containing the vectors. The proteins can be
 CC used as antigens or as compositions in the preparation of
 CC antibodies against the proteins. The polynucleotides can be used
 CC as probes for gene diagnosis, and as gene sources for gene therapy
 CC and large-scale production of proteins encoded by the cDNA. The
 CC host cells are used for the detection of ligands corresponding to
 CC the expressed proteins, and the screening of low mol.wt. medicines.
 XX
 SQ Sequence 439 BP; 89 A; 137 C; 109 G; 104 T; 0 other;
 Query Match 99.1%; Score 178.4; DB 20; Length 439;
 Best Local Similarity 99.4%; Pred. No. 1.9e-49;
 Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGGAGCGCAGTGGCCACTATGCGGTCTGGGCTGGCCCTTCCTCTTGACCTCCT 60
 Db 56 CAGGAGCGCAGTGGCCACTATGCGGTCTGGGCTGGCCCTTCCTCTTGACCTCCT 115
 QY 61 TGGCAGCTCACATGGACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTT 120
 Db 116 TGGCAGCTCACATGGACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTT 175
 QY 121 TCTGACAAAGTTCCTCTATGAGTCCAGCTTCCTGGAATGCTTGAAGAGTCTGCTCCT 180
 Db 176 TCTGACAAAGTTCCTCTATGAGTCCAGCTTCCTGGAATGCTTGAAGAGTCTGCTCCT 235
 RESULT 7
 ID AAS65519
 AC AAS65519;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #1323.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 XX
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX

PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR P-PSDB; ABG01332.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 1; SEQ ID No 1323; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 729 BP; 187 A; 169 C; 152 G; 146 T; 75 other;
 Query Match 61.0%; Score 109.8; DB 23; Length 729;
 Best Local Similarity 98.2%; Pred. No. 1.7e-26;
 Matches 111; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GGAGCGCAGTGGCCACTATGCGGTCTGGGCTGGCCCTTCCTCTTGACCTCCTTTG 62
 Db 8 GGAGCGCAGTGGCCACTATGCGGTCTGGGCTGGCCCTTCCTCTTGACCTCCTTTG 67
 QY 63 GCAGCTCACATGGACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAG 115
 Db 68 GCAGCTCACATGGACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAG 120
 RESULT 8
 ID ABK81818
 AC ABK81818;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE DNA representing lung specific gene #4.
 XX
 KW Lung specific gene; gene therapy; vaccine; lung cancer;
 KW cancer staging; cancer monitoring; cancer diagnosis;
 KW imaging lung cancer; metastases; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200218576-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 27-AUG-2001; 2001WO-US26684.
 XX
 PR 28-AUG-2000; 2000US-228378P.
 XX

PA (DIAD-) DIADEXUS INC.
XX Chen S, Macina RA, Sun Y, Recipon H;
XX WPT: 2002-434904/46.
XX New lung specific genes and their encoded proteins, useful in gene
PT therapy or as a vaccine for treating lung cancer, as well as for
PT measuring metastases of lung cancer, or staging, monitoring, diagnosing
PT or imaging lung cancer -
XX Claim 1; Page 161; 206pp; English.
XX The invention describes a new lung specific gene and it's variants. The
CC lung specific gene proteins and genes are useful in gene therapy or as a
CC vaccine for treating lung cancer. Lung specific genes are also useful for
CC staging, monitoring, diagnosing or imaging lung cancer, as well as for
CC measuring metastases of lung cancer. This sequence represents a lung
CC specific gene described in the invention.
XX Sequence 624 BP; 129 A; 175 C; 182 G; 138 T; 0 other;
SQ
Query Match 56.3%; Score 101.4; DB 24; Length 624;
Best Local Similarity 99.0%; Pred. No. 1e-23;
Matches 102; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 78 CAGGGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAAGTTCCCTCT 137
|||||
DB 314 CAGGGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCT 373
QY 138 ATGAGTCCAGCTTCTCGAATTCCTTGAAGAGCTCTGCCTCT 180
|||||
DB 374 ATGAGTCCAGCTTCTCGAATTCCTTGAAGAGCTCTGCCTCT 416
RESULT 9
ABN83971/c
ID ABN83971 standard; DNA; 6855 BP.
XX
AC ABN83971;
XX
DT 06-SEP-2002 (first entry)
XX
DE Human gene sequence #18.
XX
KW Human; brain; tonsil; hippocampus; foetal brain; diagnosis; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 4465..4695
FT /*tag= a
XX
XX WO200252005-A1.
XX
PD 04-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-JP11217.
XX
PR 22-DEC-2000; 2000JP-0389742.
XX
PA (KAZU-) KAZUSA DNA RES INST FOUND.
PA (CELE-) CELESTAR LEXICO-SCI LTD.
XX
PI Ohara O, Nagase T, Nakajima D;
XX
DR WPI: 2002-500762/53.
DR P-PSDB; ABB97951.
XX
PT Genes and their expression products cloned from human cDNA libraries
PT for treatment and diagnosis of diseases associated with their
PT expression -
XX

PS Claim 1(a); Page 136-140; 238pp; Japanese.
XX The invention relates to DNA encoding polypeptides directly cloned from
CC cDNA libraries originating in adult whole brain, human tonsil, human
CC adult hippocampus and human foetal whole brain. Polypeptides and
CC polynucleotides of the invention may be used in the investigation of
CC differential expression of the DNA sequences in normal subjects and
CC disease patients. They may also be used in the production of antibodies,
CC oligonucleotide probes and DNA chips for diagnosis and identification
CC of drugs for treatment of diseases with which the DNA sequences are
CC associated. The sequences given in records ABN83954-ABN83984 represent
XX human gene sequences of the invention.
SQ Sequence 6855 BP; 1752 A; 1535 C; 1489 G; 2079 T; 0 other;
Query Match 18.6%; Score 33.4; DB 24; Length 6855;
Best Local Similarity 57.0%; Pred. No. 1-2;
Matches 61; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 60 TTGGGAGCTCACATGGACAGGCGGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTT 119
|||||
DB 2684 TTCCCACTCCACATCCCCCAGGTTTAGTAAAGACTTTTCAAAAGCAAGGTAGGTGAAC 2625
QY 120 TTCTGCAAGTTCTCTCTATGAGTCCAGCTTCTCGGAATTCCTTGAA 166
|||||
DB 2624 TGTAGAAGAGTTCATGTTATAGTACCGCAACTTTGTATTCTCTGAA 2578
RESULT 10
AAK70447
ID AAK70447 standard; DNA; 27082 BP.
XX
AC AAK70447;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25259.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180528.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 22-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.

PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254090.
PR 05-JAN-2001; 2001US-02559678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 25259; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 27082 BP; 5963 A; 7786 C; 7711 G; 5622 T; 0 other;

Query Match

17.9%; Score 32.2; DB 22; Length 27082;

PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure; SEQ ID NO 38579; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients' own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 16596 BP; 3984 A; 4873 C; 4372 G; 3367 T; 0 other;
Query Match 17.3%; Score 31.2; DB 22; Length 16596;
Best Local Similarity 57.0%; Pred. No. 9.2;
Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
OY 16 CACTATGGGCTGGGCTGCCCTTGCTCTTGACCCCTCTTGACAGCTGCACATGG 75

DB 8094 CACCAGGCTGCCAGGGCTCTCCGGCCCTTCTGCAGCCCATGCCACCATGG 8153
OY 76 AACAGGGCCGGGTATGACTTGTTCGAACCTGAAGCTGAAGGAG 115
DB 8154 AACATGGCTGGGTGGACTGCAGGGATGGAGCTGGGGCAG 8193
RESULT 14
AAS33396/C
ID AAS33396 standard; DNA; 16596 BP.
XX
XX AAS33396;
XX
XX 04-DEC-2001 (first entry)
XX
XX DNA encoding human secreted protein, Seq ID No 679.
XX
XX Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina;
XX rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular;
XX cerebroprotective; thrombolytic; antimicrobial; ophthalmological;
XX cytostatic; Alzheimer's disease; Parkinson's disease; human cancer;
XX multiple sclerosis; cancer; hyperproliferative disorder; infection;
XX Gaucher's disease; neurological disease; cerebrovascular disorder;
XX thrombosis; wound healing; ds.
XX
XX Homo sapiens.
XX
XX W0200155326-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01347.
XX
XX 31-JAN-2000; 2000US-0179065.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-451931/48.
XX
XX New nucleic acids and polypeptides, useful for diagnosing, preventing
XX or treating medical conditions -
XX
XX Disclosure; SEQ ID No 679; 753pp; English.
XX
XX The invention relates to novel isolated nucleic acid molecules (I)
XX encoding human secreted proteins (II). (I) and (II) are used to prevent,
XX treat or ameliorate a medical condition in e.g. humans, mice, rabbits,
XX goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in
XX the prevention, treatment and diagnosis of diseases associated with
XX inappropriate expression of secreted proteins. (I) and complementary
XX sequences may also be used as DNA probes in diagnostic assays (e.g.
XX polymerase chain reactions (PCR)) to detect and quantitate the presence
XX of similar nucleic acid sequences in samples, and so which patients may
XX be in need of restorative therapy. (II) may also be used as antigens in
XX the production of antibodies and in assays to identify modulators
XX (agonists and antagonists) of the expression and activity of the secreted
XX proteins. The anti-(II) antibodies and antagonists may also be used to
XX down regulate expression and activity of (II). The anti-(II) antibodies
XX may also be used as diagnostic agents for detecting the presence of (II)
XX in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The
XX disorders include for example: immune/autoimmune diseases (e.g. HIV
XX (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
XX and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
XX melanomas, neoplasms of the breast or liver, Sezary syndrome and
XX Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
XX Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
XX cerebrovascular disorders (e.g. cardiac arrest, tachycardia,
XX angina and thrombosis), infections caused by bacteria, viruses and
XX fungi and ocular disorders (e.g. corneal infections). (I) and (II),
XX agonists, antagonists and antibodies can also be used to promote wound

CC healing, maintain organs before transplantation, and support cell culture
CC of primary tissues. AAS33043-AAS33486 represent human secreted protein
CC coding sequences, PCR primers, and related sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed.
CC specification but was obtained in electronic format directly from WIPO
CC at: ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 16596 BP; 3367 A; 4372 C; 4873 G; 3984 T; 0 other;

Query Match 17.3%; Score 31.2; DB 22; Length 16596;
Best Local Similarity 57.0%; Pred. No. 9.2;
Matches 57; Conservative 0; Mismatches 43; Indels. 0; Gaps 0;

QY 16 CACTATGGGGTGTGGCGCCCTTCTCTCTTGAACCTCTTGGCAGCTCACATGG 75

Db 8503 CACAGGCTGCCCGGCGGCTCTCCCGGCTTCTGAGCCCATGCCACCATGG 8444

QY 76 AACAGGCGGGTATGACTTTGCAACTGGAAGCTGAAGGAG 115

Db 8443 AACATGGCTGGGTGACTGCAGGATGGAGCTGGGCGAG 8404

RESULT 15

AAL36066

ID AAL36066 standard; DNA; 11749 BP.

XX

AC AAL36066;

DT 08-JAN-2002 (first entry)

XX Human musculoskeletal system related polynucleotide SEQ ID NO 2431.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system; ds.

XX Homo sapiens.

XX WO200153367-A1.

XX

PD 02-AUG-2001.

XX

XX 17-JAN-2001; 2001WO-US01338.

XX

PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 03-SEP-2000; 2000US-0229509.
PR 03-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:59:25 ; Search time 588,571 Seconds
(without alignments)
8900.373 Million cell updates/sec

Title: US-09-092-296-3
Perfect score: 180
Sequence: 1 CAGAGCGCAGTGGCCACTA.....CTTGAAAGCTCTGCTCTCT 180

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
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- 9: gb_pr.*
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- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	180	100.0	484	9	AY102070	AY102070 Homo sapi
2	178.4	99.1	422	6	AX092334	AX092334 Sequence
3	178.4	99.1	422	6	AX376174	AX376174 Sequence
4	178.4	99.1	422	6	AX403475	AX403475 Sequence
5	101.4	56.3	624	6	AX472955	AX472955 Sequence
c 6	92.4	51.3	8474	9	AL662854	AL662854 Human DNA
7	90.8	50.4	47323	9	AC005937	AC005937 Homo sapi
8	90.8	50.4	104154	2	AL773541	AL773541 Homo sapi
c 9	90.8	50.4	156272	9	AL669830	AL669830 Human DNA
10	90.8	50.4	178688	2	AL713893	AL713893 Homo sapi
11	90.8	50.4	192650	9	AB023048	AB023048 Homo sapi
12	90.8	50.4	200000	9	AF000511	AF000511 Homo sapi
13	61	33.9	349980	6	AX344571	AX344571 Sequence
c 14	55.8	31.0	349980	6	AX344553	AX344553 Sequence
c 15	55.8	31.0	349980	6	AX344554	AX344554 Sequence
c 16	44.4	24.7	175345	2	AC022301	AC022301 Mus muscu
17	43.6	24.2	132977	2	RN510020	RN510020 Rattus no
c 18	43.6	24.2	337832	2	AC099175	AC099175 Rattus no
19	36.2	20.1	185154	2	AC127110	AC127110 Rattus no
20	34.4	19.1	155406	2	AC105514	AC105514 Rattus no
21	34.2	19.0	188082	2	AC121784	AC121784 Mus muscu
22	33.6	18.7	292172	2	AC125207	AC125207 Mus muscu
c 23	33.4	18.6	6855	9	AB051446	AB051446 Homo sapi
24	33.4	18.6	97580	9	HS91N18	HS91N18 Human DNA
25	33	18.3	250442	2	AC113213	AC113213 Rattus no
26	33	18.3	349116	1	AF003003	AF003003 Mesorhizo
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c 28	32.8	18.1	158481	9	AL158063	AL158063 Human DNA
29	32.6	18.1	165618	9	AL442636	AL442636 Human DNA
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c 31	32.4	18.0	130742	2	AP005653	AP005653 Oryza sat
c 32	32.4	18.0	136733	2	AC127917	AC127917 Rattus no
33	32.2	17.9	36676	9	HS7858B16	HS7858B16 Human DNA
c 34	32	17.8	178410	2	AC125148	AC125148 Mus muscu
35	31.8	17.7	76854	2	AC130321	AC130321 Homo sapi
c 36	31.8	17.7	188121	2	AC093394	AC093394 Bos tauru
37	31.8	17.7	258446	2	AL691445	AL691445 Homo sapi
38	31.6	17.6	927556	2	AF322454	AF322454 Homo sapi
39	31.6	17.6	135171	2	AC120056	AC120056 Homo sapi
40	31.6	17.6	140678	9	AC079922	AC079922 Homo sapi
41	31.6	17.6	168421	2	AL808133	AL808133 Mus muscu
c 42	31.6	17.6	175773	2	AC113472	AC113472 Mus muscu
c 43	31.6	17.6	178531	2	AC067802	AC067802 Homo sapi
c 44	31.6	17.6	193450	2	AC111003	AC111003 Homo sapi
45	31.6	17.6	203269	2	AC080187	AC080187 Homo sapi

ALIGNMENTS

RESULT 1
AY102070
LOCUS Homo sapiens surfactant associated protein G mRNA, partial
DEFINITION sequence.
ACCESSION AY102070
VERSION AY102070.1 GI:21464498
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 484)
AUTHORS Walker, M.G. and Spiro, P.
TITLE Genes co-expressed with pulmonary surfactants

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 484)
AUTHORS Walker,M.G. and Spiro,P.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Incyte Genomics, 1475 Flamingo Way,
Sunnyvale, CA 94087-3405, USA
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
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/note="SFTPG"
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Best Local Similarity 100.0%; Pred. No. 3e-48; 0; Indels 0; Gaps 0;
Matches 180; Conservative 0; Mismatches 0;
QY 1 CAGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTCTCTGACCCCTCT 60
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QY 61 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 96 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 155
QY 121 TCTGACAACTTCTCTATGAGTCCAGCTTCTTGGAAATTCCTTGAAGCTCTGCCCTCT 180
Db 156 TCTGACAACTTCTCTATGAGTCCAGCTTCTTGGAAATTCCTTGAAGCTCTGCCCTCT 215
RESULT 2
AX092334
LOCUS AX092334 422 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 65 from Patent WO0116318.
ACCESSION AX092334
VERSION AX092334.1 GI:13444481
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 422)
AUTHORS Eaton,D.I., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 65 08-MAR-2001;
Genentech, Inc. (US)
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN
Query Match 99.1%; Score 178.4; DB 6; Length 422;
Best Local Similarity 99.4%; Pred. No. 1e-47;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTCTGACCCCTCT 60
Db 39 CAGGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTCTGACCCCTCT 98
QY 61 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 99 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158
QY 121 TCTGACAACTTCTCTATGAGTCCAGCTTCTTGGAAATTCCTTGAAGCTCTGCCCTCT 180
Db 159 TCTGACAACTTCTCTATGAGTCCAGCTTCTTGGAAATTCCTTGAAGCTCTGCCCTCT 218
RESULT 3
AX376174
LOCUS AX376174 422 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 241 from Patent WO0168848.
ACCESSION AX376174
VERSION AX376174.1 GI:19170479
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 241 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
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/organism="Homo sapiens"
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BASE COUNT 84 a 134 c 104 g 100 t
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Best Local Similarity 99.4%; Pred. No. 1e-47;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTCTGACCCCTCT 60
Db 39 CAGGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTCTGACCCCTCT 98
QY 61 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 99 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158
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Db 159 TCTGACAACTTCTCTATGAGTCCAGCTTCTTGGAAATTCCTTGAAGCTCTGCCCTCT 218
RESULT 4
AX403475
LOCUS AX403475 422 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 362 from Patent WO0073454.
ACCESSION AX403475
VERSION AX403475.1 GI:21436973
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kijavini,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 362 07-DEC-2000;
Genentech, Inc. (US)
FEATURES
source 1..422
Location/Qualifiers
/organism="Homo sapiens"
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BASE COUNT 84 a 134 c 104 g 100 t

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Db 159 TCTGACAAATTCCTCTATGAGTCCAGCTTCTTGGAAATTCCTTGAAGCTCTGCCCTCT 218
RESULT 3
AX376174
LOCUS AX376174 422 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 241 from Patent WO0168848.
ACCESSION AX376174
VERSION AX376174.1 GI:19170479
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 241 20-SEP-2001;
Genentech, Inc. (US)
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Location/Qualifiers
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BASE COUNT 84 a 134 c 104 g 100 t
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Query Match 99.1%; Score 178.4; DB 6; Length 422;
Best Local Similarity 99.4%; Pred. No. 1e-47;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTCTGACCCCTCT 60
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QY 61 TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
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RESULT 4
AX403475
LOCUS AX403475 422 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 362 from Patent WO0073454.
ACCESSION AX403475
VERSION AX403475.1 GI:21436973
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kijavini,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 362 07-DEC-2000;
Genentech, Inc. (US)
FEATURES
source 1..422
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t

On Apr 7, 2002 this sequence version replaced gi:19031750. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep XXbac-105N19 is from a CHORI-502 human bac - COX cell line library VECTOR: PTARBAC2.1		This sequence was generated from part of bacterial clone contigs constructed by the MHC Haplotype Consortium and collaborators. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6/MHC.	
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Matches		93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
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Db 56216 CAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAAGTCTCTCT 56157			
QY 138 ATGAGTCCAGCTTCTCTGGAATTCCTGAAAAGCT 171			
Db 56156 ATGAGTCCAGCTTCTCTGGAATTCCTGAAAAGCT 56123			
RESULT 7			
AC005937		47323 bp DNA linear PRI 05-NOV-1998	
LOCUS		HOMO sapiens clone UWG:370M23.002 from 6p21, complete sequence.	
DEFINITION			
ACCESSION		AC005937	
VERSION		AC005937.1 GI:3845393	
KEYWORDS		HTG.	
SOURCE		Homo sapiens.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		1 (bases 1 to 47323)	
JOURNAL		Janer, M., Guillaudoux, T., Vu, Q., Kutayavin, T., Harter, H. and Geraghty, D.E.	
TITLE		Large scale sequence analysis of the human MHC class I region	
AUTHORS		Geraghty, D.E. and Olson, M.V.	
JOURNAL		Unpublished (1998)	
REMARK		Fred Hutchinson Cancer Research Center The Clinical Research Division 1100 Fairview Ave. N., P.O. Box 19024 Seattle, WA 98109-1024	
TITLE		2 (bases 1 to 47323)	
AUTHORS		Geraghty, D.E. and Olson, M.V.	
JOURNAL		Direct Submission	
TITLE		Submitted (05-NOV-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA	

REMARK

University of Washington Human Genome Center
Box 352145 Seattle, WA 98195

Contact: Daniel E. Geraghty (geraghty@fhrc.org)

COMMENT

Overlapping Sequences:
5': UWGC:370m23.013 (Genbank Accession: AC005530)
3': UWGC:y67c112 (Genbank Accession: AC004211)

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

Double stranded (DS) coverage: 75.5%
DS or two chemistry coverage: 98.9%
Single stranded regions: 3

Sequence Validation:

This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below. Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.

	BgIII				HindIII				NsiI			
	Map	Seq	Map	Seq	Map	Seq	Map	Seq	Map	Seq	Map	Seq
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	20320.67	20855.00	1050.18	1015.00	3279.08	3231.00						
	2171.50	2147.00	7268.78	7196.00								
	2560.20	2531.00	10085.80	9992.00								
	4335.42	4269.00	11212.78	11131.00								
	2698.62	2628.00										
	1927.50	1887.00										
	3130.46	3090.00										
	2166.69	2129.00										
	2044.67	2005.00										

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22715..22957

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27835..28010

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31295..31594

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33515..33767

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34223..34290

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37372..37648

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38526..38700

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repeat_region

39583..40010

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40046..40156

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repeat_region

43194..43372

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43325

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variation

44149

/note="clonal variation with 3' overlapping clone"

variation

44451

/note="clonal variation with 3' overlapping clone"

variation

44537

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variation

44814

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variation

44965

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variation

47032

/note="clonal variation with 3' overlapping clone"

variation

47240..47256

/note="clonal variation with 3' overlapping clone"

variation

insertion of 17bp repeat"

BASE COUNT 11556 a 11489 c 12284 g 11994 t

ORIGIN

Query Match 50.4%; Score 90.8; DB 9; Length 47323;

Best Local Similarity 97.9%; Pred. No. 9.2e-19;

Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 78 CAGGCGGGGTATGACTTTCGAAGTGAAGGAGTCTTTTCGACAAATTCCTCCT 137

DB 35465 CAGGCGGGGTATGACTTTCGAAGTGAAGGAGTCTTTTCGACAAATTCCTCCT 35524

Qy 138 ATGATGCCAGTTCCTCGAATTCGTTGAAAAGCT 171

DB 35525 ATGATGCCAGTTCCTCGAATTCGTTGAAAAGCT 35558

RESULT 8

AL773541

LOCUS

DEFINITION

PROGRESS ***; in ordered pieces.

ACCESSION

AL773541

VERSION

AL773541.4

KEYWORDS

HIG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.

AL773541 104154 bp DNA linear HTG 09-AUG-2002

LOCUS Homo sapiens chromosome 6 clone Xbac-11J22, *** SEQUENCING IN

DEFINITION PROGRESS ***; in ordered pieces.

ACCESSION AL773541

VERSION AL773541.4

KEYWORDS HIG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 104154)
AUTHORS Almeida,J.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 11, 2002 this sequence version replaced gi:21621737.
COMMENT ----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BQB11J22
----- Summary Statistics
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 104135 bases at least Q40
Consensus quality: 104142 bases at least Q30
Consensus quality: 104145 bases at least Q20
Insert size: 104154; sum-of-contigs
Insert size: 110727; 1.1% error; agarose-fp
Quality coverage: 19.52x in Q20 bases; sum-of-contigs Quality
coverage: 18.64x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
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/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-11J22"
/clone_lib="DNA-arts-BAC.1-QBL.1"
1..104154
/note="assembly_fragment:00090"
BASE COUNT 26560 a 25418 c 26093 g 26083 t
ORIGIN
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Best Local Similarity 97.9%; Pred. No. 9.6e-19;
Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 78 CAGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAAGTTCTCTCT 137
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Db 67846 CAGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCT 67905
QY 138 ATGAGTCCAGCTTCTCGAATTCGTAAGAGCT 171
|||||
Db 67906 ATGAGTCCAGCTTCTCGAATTCGTAAGAGT 67939
RESULT 9
AL669830/c 156272 bp DNA linear PRI 24-APR-2002
LOCUS Human DNA sequence from clone XXbac-118E17 on chromosome 6,
DEFINITION complete sequence.
ACCESSION AL669830
VERSION AL669830.9 GI:20135762
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Johnson,C.
TITLE Direct Submission

JOURNAL Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 10, 2002 this sequence version replaced gi:20067510.
COMMENT During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em', EMBL; Sw',
SWISSPROT; Tr', TREMBL; Wp', WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep XXbac-118E17 is
from a CHORI-501 human bac - PGF cell line library VECTOR:
PTARBAC2.1
This sequence was generated from part of bacterial clone contigs
constructed by the MHC Haplotype Consortium and collaborators.
Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr6/MHC>.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-118E17"
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BASE COUNT 41135 a 37989 c 36907 g 40241 t
ORIGIN
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Query Match 50.4%; Score 90.8; DB 9; Length 156272;
Best Local Similarity 97.9%; Pred. No. 9.7e-19;
Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 78 CAGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAAGTTCTCTCT 137
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Db 25558 CAGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCT 25499
QY 138 ATGAGTCCAGCTTCTCGAATTCGTAAGAGCT 171
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Db 25498 ATGAGTCCAGCTTCTCGAATTCGTAAGAGT 25465
RESULT 10
AL713893 178688 bp DNA linear HTG 28-MAR-2002
LOCUS Homo sapiens chromosome 6 clone XXbac-307M4, *** SEQUENCING IN
DEFINITION PROGRESS ***, 6 unordered pieces.
ACCESSION AL713893
VERSION AL713893.5 GI:19847952
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sims,S.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 29, 2002 this sequence version replaced gi:19772907.
COMMENT ----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC

Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: bpG307M4
----- Summary Statistics

Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 177277 bases at least Q40
Consensus quality: 177708 bases at least Q30
Consensus quality: 177956 bases at least Q20
Insert size: 178188; sum-of-contigs
Insert size: 192613; 0.9% error; agarose-fp
Quality coverage: 8.57x in Q20 bases; sum-of-contigs Quality
Coverage: 8.00x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

* 1 37410: contig of 37410 bp in length
* 37411 37510: gap of 100 bp
* 37511 82372: contig of 44862 bp in length
* 82373 82472: gap of 100 bp
* 82473 142457: contig of 59985 bp in length
* 142458 142557: gap of 100 bp
* 142558 152859: contig of 10302 bp in length
* 152860 152959: gap of 100 bp
* 152960 172054: contig of 19095 bp in length
* 172055 172154: gap of 100 bp
* 172155 178688: contig of 6534 bp in length.

FEATURES

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/db_xref="taxon:9606"
/chromosome="6"
/clone="XXBac-307M4"
/clone_lib="CHORI-501"
1. .37410
/note="assembly_fragment:03218
fragment_chain:1"
37511. .82372
/note="assembly_fragment:00918
fragment_chain:1"
82473. .142457
/note="assembly_fragment:03231
fragment_chain:1"
142558. .152859
/note="assembly_fragment:03008
fragment_chain:1"
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fragment_chain:1"
172155. .178688
/note="assembly_fragment:03507
fragment_chain:1"
clone_end:T7
vector_side:right

BASE COUNT 46316 a 40707 c 42166 g 48998 t 501 others
ORIGIN

Query Match 50.4%; Score 90.8; DB 2; Length 178688;
Best Local Similarity 97.9%; Pred. No. 9.8e-19;
Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 78 CAGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAAGTTCTCT 137

|||||
Db 173795 CAGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATCTCT 173854

Qy 138 ATGAGTCACGCTTCCTGGAATTCGTTGAAAAGCT 171

|||||
Db 173855 ATGAGTCACGCTTCCTGGAATTCGTTGAAAAGCT 173888

RESULT 11

AB023048

LOCUS

DEFINITION

AB023048

ACCESSION

AB023048

VERSION

AB023048.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .192650

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/map="6p21.3"

/clone="53L9"

/cell_line="978SK"

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Qy 78

Db 177979

Qy 138

Db 178039

RESULT 12

LOCUS

DEFINITION

AB000511

ACCESSION

AB000511

VERSION

AB000511.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Shiina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,

Kikkawa,E., Iwata,K., Tomizawa,M., Okukuni,N., Kuwano,Y.,

Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,

Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,

Bahram,S., and Inoko,H.

Molecular dynamics of MHC genesis unraveled by sequence analysis of

the 1,796,938-bp HLA class I region

Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)

20027539

Shiina,T. and Takishima,N.

Direct Submission

Submitted (29-JAN-1999) Takashi Shiina, Tokai University School of

Medicine, Department of Molecular Life Science 2; Bohseidal,

Isehara, Kanagawa 259-1193, Japan

(E-mail:tsushima@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,

Fax:81-463-94-8884)

Location/Qualifiers

1. .192650

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/map="6p21.3"

/clone="53L9"

/cell_line="978SK"

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Qy 78

Db 177979

Qy 138

Db 178039

JOURNAL REFERENCE AUTHORS TITLE JOURNAL	Published Only in Database (1999) 2 (bases 1 to 200000) Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J. Direct Submission Submitted (21-SEP-1999) Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491, Fax:81-3-5214-8470) This sequence is conducted by Tokai University as a JST sequencing Team. Principal Investigator: Hidetoshi Inoko Ph.D Phone:+81-463-93-1121, Fax:+81-463-94-8884, The sequence is submitted by Human Genome Sequencing in ALIS project of JST Japan Science and Technology Corporation (JST) 5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan For further infomation about this sequences, please visit our sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alis.tokyo.jst.go.jp . Location/Qualifiers 1. .200000 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="6" /map="6p21.3" 108774..108864 /standard_name="D6S2088" /note="SHGC-12985:The location is between each flanking site of PCR primers." /db_xref="GDB:735268" 115648..115906 /standard_name="D6S1898" /note="WI-9418:The location is between each flanking site of PCR primers." /db_xref="GDB:678272" complement(115665..115896) /note="Cda0vhl0:The location is between each flanking site of PCR primers." /db_xref="GDB:443382" join(127993..128284,128708..128786,128938..128985,129637..129767,129949..130081,130328..130411,130596..130664,130826..130937,131154..131242,131334..131430,132032..132163,132556..132660,132922..133061,133692..133813) /gene="TFIIH" 127993..128284 /gene="TFIIH" /number=14 complement(join(128112..128284,128708..128786,128938..128985,129637..129767,129949..130081,130328..130411,130596..130664,130826..130937,131154..131242,131334..131430,132032..132163,132556..132660,132922..133058)) /gene="TFIIH" complement(join(128112..128284,128708..128786,128938..128985,129637..129767,129949..130081,130328..130411,130596..130664,130826..130937,131154..131242,131334..131430,132032..132163,132556..132660,132922..133058)) /gene="TFIIH" /codon_start=1 /product="Transcription factor II H" /protein_id="BAB63317.1" /db_xref="GI:15277224"	exon	VKRFWRQKHSS" 128708..128786 /gene="TFIIH" /number=13 128938..128985 /gene="TFIIH" /number=12 129637..129767 /gene="TFIIH" /number=11 129949..130081 /gene="TFIIH" /number=10 130328..130411 /gene="TFIIH" /number=9 130596..130664 /gene="TFIIH" /number=8 130826..130937 /gene="TFIIH" /number=7 131154..131242 /gene="TFIIH" /number=6 131334..131430 /gene="TFIIH" /number=5 132032..132163 /gene="TFIIH" /number=4 132556..132660 /gene="TFIIH" /number=3 132922..133061 /gene="TFIIH" /number=2 133692..133813 /gene="TFIIH" /number=1 join(141936..142934,143053..143202,143783..144017,14493..144711,144949..145076,145225..145469,146576..146686,147419..147584,148667..148818,148927..149022,149548..149794,149902..150089,150614..150712,150972..151119,152662..152890,153082..153184,153278..153703) /gene="DDR" 141936..142934 /gene="DDR" /number=17 142030..142159 /gene="DDR" /standard_name="D6S2203" /note="SHGC-16870:The location is between each flanking site of PCR primers." /db_xref="GDB:741215" complement(142085..142322) /note="RH18132:The location is between each flanking site of PCR primers." /db_xref="GDB:4573021" complement(142479..142740) /standard_name="D6S1851" /note="SHGC-10808:The location is between each flanking site of PCR primers." /db_xref="GDB:675281"
COMMENT	gene	complement(join(142794..142934,143053..143202,143783..144017,144493..144711,144949..145076,145225..145469,146576..146686,147419..147584,148667..148818,148927..149022,149548..149794,149902..150089,150614..150712,150972..151119,152662..152890,153082..153184,153278..153362)) /gene="DDR" complement(join(142794..142934,143053..143202,	
FEATURES source	STS	complement(join(142794..142934,143053..143202,	
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STS	STS	complement(join(142794..142934,143053..143202,	
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exon	exon	complement(join(142794..142934,143053..143202,	
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CDS	STS	complement(join(142794..142934,143053..143202,	

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145225. .145469,146576. .146686,147419. .147584,
148667. .148818,148927. .149022,149548. .149794,
149902. .150089,150614. .150712,150972. .151119,
152662. .152890,153082. .153184,153278. .153362))
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/codon_start=1
/product="Receptor tyrosine kinase"
/protein_id="BAB63318.1"
/db_xref="GI:15277225"
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SDIASSSWSDSTAARHSLSSDGCAGCPAGSVPEKEEYLQVDLRLHLVALVGT
QGRHAGSGDEFSRSLRYSRDGRPMKQKRWGEVIGNEPDEGVYKDLGPMV
RLRYFPRADRYMSVCLRYELCYLWROGLLSYAPGQTNHLSRYVINDSTDGH
TVGGQLGVQGLADGVGLDDFRKSOELRWPGDYDYGWNSNHSFSGVWEMFEFDR
LRATQAMQHCNMHTLGLARLPFGGVGEFRFRPMAMEGEPMRHNGNLGDPARAR
SVPLGGVAREFQCRFLFAGFWLLSEISFISDVYNNSSPALGTFPPAPWPPGPP
TNFSLELRPGQVPVAKAEGSPAILIGLCVAIILLLLLLIIALLMLRWLHWRLLSKA
ERRVLELTVHLSVPGDTILINRPGPREPPYOEPGRGNPHSPACVPNGSALLL
SNPAYRLLLATYARPPRGPGPTPAWAKPTNTQAYSGDMEPEKPGAPLLPPPNVS
PHYAEDIVLQGVGGNTYAPALPGAVGDGPPRVPFESRLRKEKLGSGRGEV
HLCVSDPDVSLDPLNVRKHPHLLVAVKILRPDATKNARNDFLKEYKMSRLKDP
NIIRLGVQVDDPDLMTIDIMENGDLNQLSAHQLEDKRAEGAPGQQAQGPRTSY
PMLHLVAQIAGSNRYLATLNFVHRDRLATNCLVGENFTIKIADFGSRNLYAGDIYR
VOGRAVILPMMAWECILMGKEFTTASDVWAFGVTLWEVIMLCRAQPGQLTDEQVIEN
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Query Match 50.4%; Score 90.8; DB 9; Length 200000;
Best Local Similarity 97.9%; Pred. No. 9.8e-19;
Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 78 CAGGCGGGTATGACTTTCACACTGAAGCTGAAGGAGTCTTTCTTGACAAGTCTTCCT 137
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Db 110306 CAGGCGGGTATGACTTTCACACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCT 110365
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QY 138 ATGAGTCCAGCTTCCTGGAATTCGTTGAAAAGCT 171
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Db 110366 ATGAGTCCAGCTTCCTGGAATTCGTTGAAAAGCT 110399
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RESULT 13
AX344571 AX344571 349980 bp DNA linear PAT 01-FEB-2002
LOCUS Sequence 22 from Patent WO0200932.
DEFINITION AX344571
ACCESSION AX344571
VERSION AX344571.1 GI:18492457
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Olek.A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 22 03-JAN-2002;
Epigenomics AG (DE)
FEATURES Location/Qualifiers
source 1. .349980
/organism="synthetic construct"

/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows--seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-Original length of seq 2: 3.673778 <223>-split as follows--seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 2.749.980-seq 23 2.700.001 3.049.980-seq 24 3.000.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.673.778"

BASE COUNT 91992 a 5703 c 86514 g 165771 t
ORIGIN

Query Match 33.9%; Score 61; DB 6; Length 349980;
Best Local Similarity 78.3%; Pred. No. 6.7e-09;
Matches 73; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 79 AGGCGCGGTATGACTTTCACACTGAAGCTGAAGGAGTCTTTCTTGACAAGTCTTCCTA 138
|||||
Db 54267 AGGCGCGGTATGACTTTCACACTGAAGCTGAAGGAGTCTTTCTGATAAATTTTTTTA 54326
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QY 139 TGAGTCCAGCTTCCTGGAATTCGTTGAAAAGCT 171
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Db 54327 TGAGTTCAGTTTTTTTGGAAATGTTTGAAGAAGGT 54359
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RESULT 14
AX344553/c AX344553 349980 bp DNA linear PAT 01-FEB-2002
LOCUS Sequence 4 from Patent WO0200932.
DEFINITION AX344553
ACCESSION AX344553
VERSION AX344553.1 GI:18492439
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Olek.A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 4 03-JAN-2002;
Epigenomics AG (DE)
FEATURES Location/Qualifiers
source 1. .349980
/organism="synthetic construct"

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Query Match          31.0%; Score 55.8; DB 6; Length 349980;
Best Local Similarity 75.8%; Pred. No. 3.5e-07;
Matches 69; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 78 CAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAAGTTCTCTCT 137
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Db 319513 CAAACCGGAATATAACTTTTACAACATAAACTAAAAAAATCTTTTCTAACAAATTCCTCT 319454

Qy 138 ATGAGTCCAGCTTCCTGGAATTGCTTGAAAA 168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319453 ATAAATCCAACCTTCCTAAAATTAATTAATAAA 319423

RESULT 15
AX344554/c
LOCUS      AX344554          349980 bp      DNA      linear      PAT 01-FEB-2002
DEFINITION Sequence 5 from Patent WO0200932.
ACCESSION  AX344554
VERSION     AX344554.1  GI:18492440
KEYWORDS    .
SOURCE      synthetic construct.
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Olek A., Piepenbrock,C. and Berlin,K.
TITLE       Diagnosis of known genetic parameters within the mhc
JOURNAL     Patent: WO 0200932-A 5 03-JAN-2002;
            Epigenomics AG (DE)
FEATURES    Location/Qualifiers
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               /db_xref="taxon:32630"
               /note="Chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-Original length of seq 2: 3.673778 <223>-split as follows.-seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 2.749.980-seq 23 2.700.001 3.049.980-seq 24 3.000.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.673.778"
BASE COUNT  92349 a 5068 c 82248 g 170315 t
ORIGIN

Query Match          31.0%; Score 55.8; DB 6; Length 349980;
Best Local Similarity 75.8%; Pred. No. 3.5e-07;
Matches 69; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Db 19513 CAAACCGGAATATAACTTTTACAACATAAACTAAAAAAATCTTTTCTAACAAATTCCTCT 19454

Qy 138 ATGAGTCCAGCTTCCTGGAATTGCTTGAAAA 168
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Db 19453 ATAAATCCAACCTTCCTAAAATTAATTAATAAA 19423

Search completed: May 1, 2003, 04:24:01
Job time : 1127.57 secs
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 04:34:36 ; Search time 61.534 Seconds
(without alignments)
4397.425 Million cell updates/sec

Title: US-09-092-296-2

Perfect score: 229
Sequence: 1 ACCGGACTTCAGTGTCTCC.....CCATCTCCCTTCAGGGACCA 229

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 746064 seqs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*

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2: /cgn2_6/ptodata/1/pubpna/FCI_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PTUS_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	228	99.6	239	9	US-09-092-296-1
3	218	95.2	413	9	US-09-092-296-6
4	218	95.2	422	9	US-09-092-598-362
5	218	95.2	422	9	US-09-989-293A-362
6	218	95.2	422	9	US-10-063-547-65
7	218	95.2	422	9	US-09-989-735-362
8	218	95.2	422	9	US-09-990-444-362
9	218	95.2	422	9	US-09-989-730-362
10	218	95.2	422	9	US-09-990-436-362
11	218	95.2	422	9	US-09-991-181-362
12	218	95.2	422	9	US-09-993-687-362
13	218	95.2	422	9	US-09-989-734-362
14	218	95.2	422	9	US-09-997-653-362
15	218	95.2	422	9	US-10-174-590-241
16	218	95.2	422	9	US-10-176-758-241
17	218	95.2	422	9	US-10-063-616-65
18	218	95.2	422	9	US-10-175-737-241
19	218	95.2	422	9	US-09-993-667-362

20	218	95.2	422	9	US-10-063-502-65	Sequence 65, Appl
21	218	95.2	422	9	US-10-173-706-241	Sequence 241, App
22	218	95.2	422	9	US-10-175-738-241	Sequence 241, App
23	218	95.2	422	9	US-10-175-752-241	Sequence 241, App
24	218	95.2	422	9	US-10-176-482-241	Sequence 241, App
25	218	95.2	422	9	US-10-176-757-241	Sequence 241, App
26	218	95.2	422	9	US-10-176-913-241	Sequence 241, App
27	218	95.2	422	9	US-10-180-552-241	Sequence 241, App
28	218	95.2	422	9	US-10-180-557-241	Sequence 241, App
29	218	95.2	422	9	US-09-990-438-362	Sequence 362, App
30	218	95.2	422	9	US-09-990-562-362	Sequence 362, App
31	218	95.2	422	9	US-09-997-428-362	Sequence 362, App
32	218	95.2	422	9	US-09-997-666-362	Sequence 362, App
33	218	95.2	422	9	US-10-173-700-241	Sequence 241, App
34	218	95.2	422	9	US-10-174-572-241	Sequence 241, App
35	218	95.2	422	9	US-10-174-579-241	Sequence 241, App
36	218	95.2	422	9	US-10-174-582-241	Sequence 241, App
37	218	95.2	422	9	US-10-174-588-241	Sequence 241, App
38	218	95.2	422	9	US-10-175-739-241	Sequence 241, App
39	218	95.2	422	9	US-10-175-740-241	Sequence 241, App
40	218	95.2	422	9	US-10-175-743-241	Sequence 241, App
41	218	95.2	422	9	US-10-176-488-241	Sequence 241, App
42	218	95.2	422	9	US-10-176-492-241	Sequence 241, App
43	218	95.2	422	9	US-10-176-747-241	Sequence 241, App
44	218	95.2	422	9	US-10-176-750-241	Sequence 241, App
45	218	95.2	422	9	US-10-176-985-241	Sequence 241, App

ALIGNMENTS

RESULT 1
US-09-092-296-2
; Sequence 2, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; NAME/KEY: base_polymorphism
; LOCATION: 200
; OTHER INFORMATION: /note= " N' represents an A or G or
; OTHER INFORMATION: T or C polymorphism at this position"
US-09-092-296-1

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Best Local Similarity 100.0%; Pred. No. 4.1e-68;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCCCCTTGCTCTCTCTTGACCTCTCTTGCGAGCTCACATGGAACAGGCGGGGTATGAC 120
Db 61 GCCCCTTGCTCTCTCTTGACCTCTCTTGCGAGCTCACATGGAACAGGCGGGGTATGAC 120
QY 121 TTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
Db 121 TTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
QY 181 GGAATTGCTGAAAGTCTGCCCTCCCTCCATCTCCCTTCCAGGACCA 229
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RESULT 2
US-09-092-296-1
; Sequence 1, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; NAME/KEY: base_polymorphism
; LOCATION: 200
; OTHER INFORMATION: /note= " N' represents an A or G or
; OTHER INFORMATION: T or C polymorphism at this position"
US-09-092-296-1

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US-09-092-296-6
; Sequence 6, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
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; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-092-296-6

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QY 61 GCCCCTTGTCCTCTTGGACCTCTTGGCAGCTCACATGGAACAGGCGCGGTATGAC 120
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QY 121 TTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
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QY 181 GGAATTGCTGAAAG-TCTGGCTCTCTCTCCATCTCCCTTCAGGACCA 229
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RESULT 4
US-09-092-598-362
; Sequence 362, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544

; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 218; DB 9; Length 422;

Best Local Similarity 99.6%; Pred. No. 2.8e-64;

Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 60

Db 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 71

Qy 61 GCCCTTGTCTCTCTTGTGACCTCTTTGGCAGCTCACATGGAACAGGCGGGGTATGAC 120

Db 72 GCCCTTGTCTCTCTTGTGACCTCTTTGGCAGCTCACATGGAACAGGCGGGGTATGAC 131

Qy 121 TTGCACTGAAGCTGAAGGAGTCTTTTCTGACAAATCTCTCTATGATCCAGCTTCT 180

Db 132 TTGCACTGAAGCTGAAGGAGTCTTTTCTGACAAATCTCTCTATGATCCAGCTTCT 191

Qy 181 GGAATGCTTGAAAG-TCTGGCTCTCTCCATCTCTCTCTCCATCTCTCTCAGGACCA 229

Db 192 GGAATGCTTGAAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAGGACCA 241

RESULT 5

US-09-989-293A-362

; Sequence 362, Application US/09989293A

; Patent No. US20020177164A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerriksen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C66

; CURRENT APPLICATION NUMBER: US/09/989, 293A

; PRIOR FILING DATE: 2001-11-20

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

1	PRIOR APPLICATION NUMBER: 60/065186	2	PRIOR FILING DATE: 1997-11-12	3	PRIOR FILING DATE: 1998-06-16
4	PRIOR APPLICATION NUMBER: 60/065311	5	PRIOR FILING DATE: 1997-11-12	6	PRIOR FILING DATE: 1998-06-16
7	PRIOR APPLICATION NUMBER: 60/065770	8	PRIOR FILING DATE: 1997-11-13	9	PRIOR FILING DATE: 1998-06-17
10	PRIOR APPLICATION NUMBER: 60/075945	11	PRIOR FILING DATE: 1997-11-24	12	PRIOR FILING DATE: 1998-06-17
13	PRIOR APPLICATION NUMBER: 60/078910	14	PRIOR FILING DATE: 1998-02-25	15	PRIOR FILING DATE: 1998-06-17
16	PRIOR APPLICATION NUMBER: 60/083322	17	PRIOR FILING DATE: 1998-03-20	18	PRIOR FILING DATE: 1998-06-17
19	PRIOR APPLICATION NUMBER: 60/084600	20	PRIOR FILING DATE: 1998-04-28	21	PRIOR FILING DATE: 1998-06-17
22	PRIOR APPLICATION NUMBER: 60/085007	23	PRIOR FILING DATE: 1998-05-07	24	PRIOR FILING DATE: 1998-06-17
25	PRIOR APPLICATION NUMBER: 60/087106	26	PRIOR FILING DATE: 1998-05-28	27	PRIOR FILING DATE: 1998-06-17
28	PRIOR APPLICATION NUMBER: 60/087607	29	PRIOR FILING DATE: 1998-06-02	30	PRIOR FILING DATE: 1998-06-17
31	PRIOR APPLICATION NUMBER: 60/087609	32	PRIOR FILING DATE: 1998-06-02	33	PRIOR FILING DATE: 1998-06-18
34	PRIOR APPLICATION NUMBER: 60/087759	35	PRIOR FILING DATE: 1998-06-02	36	PRIOR FILING DATE: 1998-06-18
37	PRIOR APPLICATION NUMBER: 60/087827	38	PRIOR FILING DATE: 1998-06-03	39	PRIOR FILING DATE: 1998-06-18
40	PRIOR APPLICATION NUMBER: 60/088021	41	PRIOR FILING DATE: 1998-06-04	42	PRIOR FILING DATE: 1998-06-19
43	PRIOR APPLICATION NUMBER: 60/088025	44	PRIOR FILING DATE: 1998-06-04	45	PRIOR FILING DATE: 1998-06-19
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49	PRIOR APPLICATION NUMBER: 60/088028	50	PRIOR FILING DATE: 1998-06-04	51	PRIOR FILING DATE: 1998-06-22
52	PRIOR APPLICATION NUMBER: 60/088029	53	PRIOR FILING DATE: 1998-06-04	54	PRIOR FILING DATE: 1998-06-22
55	PRIOR APPLICATION NUMBER: 60/088030	56	PRIOR FILING DATE: 1998-06-04	57	PRIOR FILING DATE: 1998-06-22
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61	PRIOR APPLICATION NUMBER: 60/088326	62	PRIOR FILING DATE: 1998-06-04	63	PRIOR FILING DATE: 1998-06-23
64	PRIOR APPLICATION NUMBER: 60/088167	65	PRIOR FILING DATE: 1998-06-05	66	PRIOR FILING DATE: 1998-06-24
67	PRIOR APPLICATION NUMBER: 60/088202	68	PRIOR FILING DATE: 1998-06-05	69	PRIOR FILING DATE: 1998-06-24
70	PRIOR APPLICATION NUMBER: 60/088212	71	PRIOR FILING DATE: 1998-06-05	72	PRIOR FILING DATE: 1998-06-24
73	PRIOR APPLICATION NUMBER: 60/088217	74	PRIOR FILING DATE: 1998-06-05	75	PRIOR FILING DATE: 1998-06-24
76	PRIOR APPLICATION NUMBER: 60/088655	77	PRIOR FILING DATE: 1998-06-09	78	PRIOR FILING DATE: 1998-06-24
79	PRIOR APPLICATION NUMBER: 60/088734	80	PRIOR FILING DATE: 1998-06-10	81	PRIOR FILING DATE: 1998-06-24
82	PRIOR APPLICATION NUMBER: 60/088738	83	PRIOR FILING DATE: 1998-06-10	84	PRIOR FILING DATE: 1998-06-24
85	PRIOR APPLICATION NUMBER: 60/088742	86	PRIOR FILING DATE: 1998-06-10	87	PRIOR FILING DATE: 1998-06-24
88	PRIOR APPLICATION NUMBER: 60/088810	89	PRIOR FILING DATE: 1998-06-10	90	PRIOR FILING DATE: 1998-06-24
91	PRIOR APPLICATION NUMBER: 60/088824	92	PRIOR FILING DATE: 1998-06-10	93	PRIOR FILING DATE: 1998-06-24
94	PRIOR APPLICATION NUMBER: 60/088826	95	PRIOR FILING DATE: 1998-06-10	96	PRIOR FILING DATE: 1998-06-24
97	PRIOR APPLICATION NUMBER: 60/088858	98	PRIOR FILING DATE: 1998-06-11	99	PRIOR FILING DATE: 1998-06-25
100	PRIOR APPLICATION NUMBER: 60/088861	101	PRIOR FILING DATE: 1998-06-11	102	PRIOR FILING DATE: 1998-06-25
103	PRIOR APPLICATION NUMBER: 60/088876	104	PRIOR FILING DATE: 1998-06-11	105	PRIOR FILING DATE: 1998-06-25
106	PRIOR APPLICATION NUMBER: 60/089105	107	PRIOR FILING DATE: 1998-06-12	108	PRIOR FILING DATE: 1998-06-25
109	PRIOR APPLICATION NUMBER: 60/089440	110	PRIOR FILING DATE: 1998-06-16	111	PRIOR FILING DATE: 1998-06-26
112	PRIOR APPLICATION NUMBER: 60/089512	113	PRIOR FILING DATE: 1998-06-16	114	PRIOR FILING DATE: 1998-06-26

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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGCACATGGAACAGCGCGGTATGAC 120
Db 12 ACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGCACATGGAACAGCGCGGTATGAC 131
QY 61 GCCCCTGTCCCTCTTGACCTCTCTGGCAGCTCACATGGAACAGCGCGGTATGAC 120
Db 72 GCCCCTGTCCCTCTTGACCTCTCTGGCAGCTCACATGGAACAGCGCGGTATGAC 131
QY 121 TTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
Db 132 TTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 191
QY 181 GGAATTGCTTGAAGAAG-TCTGCGCTCTCTCCATCTCCCTTCAGGAGCA 229
Db 192 GGAATTGCTTGAAGAAGCTCTGCGCTCTCTCCATCTCCCTTCAGGAGCA 241

RESULT 6
; Sequence 65, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Falvaroff, Ellen
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063.547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-547-65

Query Match          95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGCACATGGAACAGCGGTATGAC 60
Db 12 ACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGCACATGGAACAGCGGTATGAC 71
QY 61 GCCCCTGTCCCTCTTGACCTCTCTGGCAGCTCACATGGAACAGCGCGGTATGAC 120
Db 72 GCCCCTGTCCCTCTTGACCTCTCTGGCAGCTCACATGGAACAGCGCGGTATGAC 131
QY 121 TTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
Db 132 TTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 191
QY 181 GGAATTGCTTGAAGAAG-TCTGCGCTCTCTCCATCTCCCTTCAGGAGCA 229
Db 192 GGAATTGCTTGAAGAAGCTCTGCGCTCTCTCCATCTCCCTTCAGGAGCA 241
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Db 12 ACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGCACATGATGGGTCTGGGCT 71
QY 61 GCCCCTGTCCCTCTTGACCTCTCTGGCAGCTCACATGGAACAGCGCGGTATGAC 120
Db 72 GCCCCTGTCCCTCTTGACCTCTCTGGCAGCTCACATGGAACAGCGCGGTATGAC 131
QY 121 TTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
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QY 181 GGAATTGCTTGAAGAAG-TCTGCGCTCTCTCCATCTCCCTTCAGGAGCA 229
Db 192 GGAATTGCTTGAAGAAGCTCTGCGCTCTCTCCATCTCCCTTCAGGAGCA 241

RESULT 7
US-09-989-735-362
; Sequence 362, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989.735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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; PRIOR APPLICATION NUMBER: 60/089801
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089907
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089908
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089947
 ; PRIOR FILING DATE: 1998-06-19
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 ; PRIOR APPLICATION NUMBER: 60/090246
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 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091478
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091544
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982

; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09
 Query Match 95.28; Score 218; DB 9; Length 422;
 Best local Similarity 99.64; Pred. No. 2.8e-64; Indels 1; Gaps 1;
 Matches 229; Conservative 0; Mismatches 0;
 QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 60
 |||||
 Db 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 71
 |||||
 QY 61 GCCCCTTGTCTCCCTCTTGCACCTCTTGCAGCTCAGATGGAACAGGCGCGGTATGAC 120
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 Db 72 GCCCCTTGTCTCCCTCTTGCACCTCTTGCAGCTCAGATGGAACAGGCGCGGTATGAC 131
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 QY 121 TTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGATCCAGTCTTCT 180
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 Db 132 TTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGATCCAGTCTTCT 191
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 QY 181 GGAATTCCTTGAAGAAG-TCTGCCTCTCTCCATCTCCCTTCAGGGACCA 229
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 Db 192 GGAATTCCTTGAAGAAGCTCTGCCCTCTCCATCTCCCTTCAGGGACCA 241
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RESULT 9
 US-09-989-730-362
 ; Sequence 362, Application US/09989730
 ; Publication No. US20020197674A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC69
 ; CURRENT APPLICATION NUMBER: US/09/989,730
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
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 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20

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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match	95.2%	Score 218;	DB 9;	Length 422;
Best Local Similarity	99.6%;	Pred. No. 2.8e-64;		
Matches 229;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
QY	1	ACGGGACTTCAGTGTCTCTCCATCCGAGAGCGGACATGCGGCATCTGGGCTCTGGGCT	60	
Db	12	ACGGGACTTCAGTGTCTCTCCATCCGAGAGCGGACATGCGGCATCTGGGCTCTGGGCT	71	
QY	61	GCCTCTGTCTCTCTCTTGGACCTCTTGGCAGCTCACATGGAACAGGCCGGGTTATGAC	120	
Db	72	GCCTCTGTCTCTCTCTTGGACCTCTTGGCAGCTCACATGGAACAGGCCGGGTTATGAC	131	
QY	121	TTTGCAACTGAAGCTGAAGGAGTCTTTCTTGACAAATTCCTCTATGATGATCAGGCTTCCT	180	
Db	132	TTTGCAACTGAAGCTGAAGGAGTCTTTCTTGACAAATTCCTCTATGATGATCAGGCTTCCT	191	
QY	181	GGAATTGCTTGAAGAAG-TCCTGGCTCTCTCTCCATCTCCCTTCAGGGACCA	229	
Db	192	GGAATTGCTTGAAGAAGCTCTGGCTCTCTCTCCATCTCCCTTCAGGGACCA	241	

RESULT 10

US-09-990-436-362

Sequence 362, Application US/09990436

Publication No. US20020198148A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC14

CURRENT APPLICATION NUMBER: US/09/990.436

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

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PRIOR FILING DATE: 1997-11-13

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; PRIOR APPLICATION NUMBER: 60/089538
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 95.28; Score 218; DB 9; Length 422;
Best Local Similarity 99.68; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGGACGTGGCCACTATGGGCTCTGGGCT 60
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Db 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGGACGTGGCCACTATGGGCTCTGGGCT 71
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QY 61 GCCCTTGTCTCTCTTGACCTCTTGGCAGCTCACATGGAACAGGCCGGGTATGAC 120
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QY 121 TTGCACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 180
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Db 132 TTGCACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 191
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QY 181 GGAATTGCTTGAAGAAG-TCTGCCTCTCTCCATCTCCCTTCAGGACCA 229
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Db 192 GGAATTGCTTGAAGAAGCTCTGCCTCTCTCCATCTCCCTTCAGGACCA 241
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RESULT 11
US-09-991-181-362
; Sequence 362, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kiljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

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2 PRIOR FILING DATE: 1997-11-12
3 PRIOR APPLICATION NUMBER: 60/065311
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11 PRIOR APPLICATION NUMBER: 60/083322
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146 PRIOR FILING DATE: 1998-06-26

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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          95.2%  Score 218;  DB 9;  Length 422;
Best Local Similarity 99.6%  Pred. No. 2.8e-64;
Matches 229;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 1;

QY 1 ACCGGGACTTCAGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 60
   |||||
Db 12 ACCGGGACTTCAGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 71
   |||||

QY 61 GCCCCTTGTCCTCTCTTGGACCCCTCTTGGCAGCTTCACATGGAAACAGCGCGGTATGAC 120
   |||||
Db 72 GCCCCTTGTCCTCTCTTGGACCCCTCTTGGCAGCTTCACATGGAAACAGCGCGGTATGAC 131
   |||||

QY 121 TTGCACTCAAGCTGAAGGAGTCTTTCTGACAAATCTCTCTATGAGTCCAGCTTCCT 180
   |||||
Db 132 TTGCACTCAAGCTGAAGGAGTCTTTCTGACAAATCTCTCTATGAGTCCAGCTTCCT 191
   |||||

QY 181 GGAATTCCTGAAAAG-TCTGCCCTCTCTCTCCATCTCCCTTCAGGGACCA 229
   |||||
Db 192 GGAATTCCTGAAAAGCTCTGCCCTCTCTCCATCTCTCTTCAGGGACCA 241
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RESULT 12
US-09-993-687-362
; Sequence 362, Application US/09993687
; Publication No. US2002019819A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C11
; CURRENT APPLICATION NUMBER: US/09/993,687
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; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
Query Match 95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 ACCGGGACTTCAGTGCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 60
Db 12 ACCGGGACTTCAGTGCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 71
Qy 61 GCCCTTGTCTCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACAGGCGCGGTATGAC 120
Db 72 GCCCTTGTCTCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACAGGCGCGGTATGAC 131
Qy 121 TTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
Db 132 TTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 191
Qy 181 GGAATTGCTTGAAGAAG-TCTGGCTCTCTCCATCTCCCTTCAGGGACCA 229
Db 192 GGAATTGCTTGAAGAAGTCTGCTCTCTCCATCTCCCTTCAGGGACCA 241
RESULT 13
US-09-989-734-362
; Sequence 362, Application US/09989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730P1C64
;; CURRENT APPLICATION NUMBER: US/09/989,734
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
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, PRIOR APPLICATION NUMBER: 60/092182
, PRIOR FILING DATE: 1998-07-09

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Query Match 95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.8e-64;

QY	1	ACCGGAGCTTCAGTGTCTCTCCATCCACGAGAGCGAGTGGCCACTATGGGCTCTGGGCT	60
Db	12	ACCGGAGCTTCAGTGTCTCTCTCCATCCACGAGAGCGAGTGGCCACTATGGGCTCTGGGCT	71
QY	61	GCCCTTTGCTCCCTCTCTTGACCCCTCCCTGGCAGCTCACTNGAACAGGCGCGGTATGAC	120
Db	72	GCCCTTTGCTCCCTCTCTTGACCCCTCCCTGGCAGCTCACTNGAACAGGCGCGGTATGAC	131
QY	121	TTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT	180
Db	132	TTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT	191
QY	181	GGAATTCGTTGAAAG-TCTGCCCTCTCTCCATCTCCCTTCAGGACCA	229
Db	192	GGAATTCGTTGAAAGCTCTGCCCTCTCTCTCCATCTCCCTTCAGGACCA	441

RESULT 14

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US-09-997-653-362
; Sequence 362, Application US/09997653
; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guney, Austin L.
; APPLICANT: Kljavin, Ivair J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Peoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

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; PRIOR APPLICATION NUMBER: 60/088824
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ACCGGACCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCGCACTATGGGTCTGGGCT 60
Db 12 ACCGGACCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCGCACTATGGGTCTGGGCT 71

Qy 61 GCCCCTTGTCTCTCTTTGACCTCTTTGGCAGTCCATCGAACAGGCGGGGTATGAC 120
Db 72 GCCCCTTGTCTCTCTTTGACCTCTTTGGCAGTCCATCGAACAGGCGGGGTATGAC 131

Qy 121 TTGCAACTGAAGCTGAAGGAGTCTTTTTCACAAATTCCTCTATGATCCAGCTTCT 180
Db 132 TTGCAACTGAAGCTGAAGGAGTCTTTTTCACAAATTCCTCTATGATCCAGCTTCT 191

Qy 181 GGAAATGGTTGAAAAG-TCGTGCTCTCTCTCCATCTCCCTTCAGGACCA 229
Db 192 GGAAATGGTTGAAAAGCTGTGCTCTCTCTCCATCTCCCTTCAGGACCA 241

RESULT 15
US-10-174-590-241
; Sequence 241, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME


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; FILE REFERENCE: P3430RIC42
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; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
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; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-174-590-241
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Query Match      95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 60
Db 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 71

QY 61 GCCCTTGCTCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACAGGCCGGGTATGAC 120
Db 72 GCCCTTGCTCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACAGGCCGGGTATGAC 131

QY 121 TTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCT 180
Db 132 TTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCT 191

QY 181 GGAATTGCTGAAAAG-TCTGCTCTCTCTCTCCATCTCCCTTCAGGGACCA 229
Db 192 GGAATTGCTGAAAAGCTCTGCTCTCTCTCTCCATCTCCCTTCAGGGACCA 241
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Search completed: May 1, 2003, 05:17:10
Job time : 63.534 secs

GenCore version 5.1.5
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OM nucieic - nucleic search, using sw model

Run on: May 1, 2003, 03:08:45 ; Search time 1146.82 Seconds
(without alignments)
3233.964 Million cell updates/sec

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Perfect score: 229
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3:	em_estin:*
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5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_estl:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estom:*
16:	em_estom:*
17:	gb_gss:*
18:	em_gss_hum:*
19:	em_gss_inv:*
20:	em_gss_pln:*
21:	em_gss_vrt:*
22:	em_gss_fun:*
23:	em_gss_man:*
24:	em_gss_mus:*
25:	em_gss_other:*
26:	em_gss_pro:*
27:	em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

c 1	216.4	94.5	449	10 AW293443	AW293443 UI-H-BI2-
2	216.4	94.5	830	13 BI759796	BI759796 603045679
3	215	93.9	456	12 BG506690	BG506690 601861290
c 4	213	93.0	422	12 BF002050	BF002050 7998c11.x
5	132.2	57.7	895	13 BI820029	BI820029 603037210
6	131	57.2	865	13 BI820110	BI820110 603037110

c	7	113	49.3	404	9	A1857998	A1857998 w169b01.x
8	94	41.0	521	10	BB533837	BB533837 BB533837	
9	94	41.0	522	10	BB664284	BB664284 BB664284	
10	92.2	40.3	361	12	BF521842	BF521842 UI-R-C2p-	
c 11	75.4	32.9	552	17	AQ718761	AQ718761 HS_5511_B	
c 12	61.8	27.0	328	9	AI136523	AI136523 UI-R-C2p-	
c 13	45.6	19.9	506	17	A2241329	A2241329 RPCI-23-7	
c 14	45.6	19.9	633	17	A2079350	A2079350 RPCI-23-4	
15	36	15.7	754	12	BG686317	BG686317 602638230	
16	36	15.7	1020	13	BM477469	BM477469 AGENCOURT	
17	35	15.3	348	14	F06958	F06958 HSC10C101.n	
18	35	15.3	509	17	AQ838514	AQ838514 HS_5011_A	
19	35	15.3	1019	13	BM474221	BM474221 AGENCOURT	
c 20	34.6	15.1	261	10	BB411111	BB411111 BB411111	
c 21	34.4	15.0	238	9	AA376266	AA376266 EST88915	
c 22	34.4	15.0	264	14	BQ377407	BQ377407 IL5-UM007	
c 23	34.4	15.0	412	9	AA769782	AA769782 ah71b05.s	
c 24	34.4	15.0	458	9	AI632159	AI632159 ts85e12.x	
c 25	34.4	15.0	470	9	AI803529	AI803529 tc42h11.x	
26	34.4	15.0	516	10	BE613876	BE613876 601504191	
c 27	34.4	15.0	543	10	AW851149	AW851149 IL3-CT022	
28	34.4	15.0	753	13	BI911665	BI911665 603064838	
29	34.4	15.0	783	10	BE563718	BE563718 601335355	
30	34.4	15.0	785	13	BI193645	BI193645 602946554	
31	34.4	15.0	788	12	BG762871	BG762871 602735108	
32	34.4	15.0	828	12	BG768039	BG768039 602743815	
33	34.4	15.0	837	13	BM449774	BM449774 AGENCOURT	
34	34.4	15.0	871	14	BQ956320	BQ956320 AGENCOURT	
35	34.4	15.0	931	12	BF689789	BF689789 602186518	
36	34.4	15.0	954	14	BQ220846	BQ220846 AGENCOURT	
37	34.4	15.0	959	14	BQ940113	BQ940113 AGENCOURT	
38	34.4	15.0	999	9	AL551231	AL551231 AL551231	
39	34.4	15.0	1013	14	BQ953477	BQ953477 AGENCOURT	
40	34.4	15.0	1061	14	BQ052186	BQ052186 AGENCOURT	
41	34.4	15.0	1129	13	BM464458	BM464458 AGENCOURT	
42	34.4	15.0	1138	13	BM564409	BM564409 AGENCOURT	
43	34.4	15.0	1232	14	BM911289	BM911289 AGENCOURT	
c 44	34	14.8	271	17	BH244391	BH244391 ATZEB57TF	
45	34	14.8	637	17	BH244484	BH244484 ATZEE11TF	

ALIGNMENTS

RESULT 1
LOCUS AW293443/c
DEFINITION UI-H-BI2-ahm-c-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens CDNA clone
IMAGE:2727182 3', mRNA sequence.
ACCESSION AW293443
VERSION AW293443.1 GI:67000079
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 449)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone Distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/ILNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
PolyA-res.

FEATURES

Location/Qualifiers

source	1. 449		/organism="Homo sapiens"	
	/db_xref="taxon:9606"		/clone="IMAGE:2727182"	
	/clone_lib="NCI_CGAP_Sub4"		/lab_host="DH10B (Life Technologies)"	
	/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_Sub4 library is a subtracted library derived from the NCI_CGAP_Sub2 library which is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from BL. B1 constitutes a mixture of 21 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Le12, NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6, NCI_CGAP_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:			
	NCI_CGAP_Kid3 pool 1 : LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 : LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1329312-1325831, 1471368-1472903, 1492104-1493255) NCI_CGAP_Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4 pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI_CGAP_Pr22 pool 1 : LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615) NCI_CGAP_Co10 pool 1 : LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351) [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]			
	TAG_LIB="NCI_CGAP_Co4		TAG_TISSUE="colon	
	TAG_SEQ="CTTCG"			
BASE COUNT	104 a	108 c	134 g	103 t
ORIGIN				
	Query Match 94.5%; Score 216.4; DB 10; Length 449;			
	Best Local Similarity 99.1%; Pred. No. 1.1e-51;			
	Matches 228; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
QY	1	ACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCCTGGGCT	60	
Db	433	ACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCCTGGGCT	374	
QY	61	GCCCCCTGTCTCTTGTAGCCCTCTTGGCAGCTCACAATGGACAGGCGCGGATGAC	120	
Db	373	GCCCCCTGTCTCTTGTAGCCCTCTTGGCAGCTCACAATGGACAGGCGCGGATGAC	314	
QY	121	TTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCATAGTCCAGCTTCTCT	180	
Db	313	TTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCATAGTCCAGCTTCTCT	254	
QY	181	GGAATTCCTGAAAAG-TCTGCCCTCCCTCCATCTCCCTTCAGGACCA	229	
Db	253	GGAATTCCTGAAAAGCTCTGCCCTCCCTCCATCTCCCTTCAGGACCA	204	
RESULT 2				
BI759796	830 bp mRNA linear EST 25-SEP-2001			
LOCUS	603045679F1 NIH_MGC_116 Homo sapiens cdna clone IMAGE:5186107 5',			
DEFINITION	mRNA sequence.			
ACCESSION	BI759796			
VERSION	BI759796.1 GI:15751374			
KEYWORDS	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.			
TITLE	1 (bases 1 to 830)			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: ccapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11464 row: m column: 20 High quality sequence stop: 432.			
FEATURES	Location/Qualifiers			
	1..830			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:5186107"			
	/clone_lib="NIH_MGC_116"			
	/lab_host="DH10B"			
	/note="Organ: pooled colon, kidney, stomach; Vector: PCMV-SPO76; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."			
BASE COUNT	175 a	276 c	210 g	168 t
ORIGIN				
	Query Match 94.5%; Score 216.4; DB 13; Length 830;			
	Best Local Similarity 99.1%; Pred. No. 1.4e-51;			
	Matches 228; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
QY	1	ACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCCTGGGCT	60	
Db	35	ACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCCTGGGCT	94	
QY	61	GCCCCCTGTCTCTTGTAGCCCTCTTGGCAGCTCACAATGGACAGGCGCGGATGAC	120	
Db	95	GCCCCCTGTCTCTTGTAGCCCTCTTGGCAGCTCACAATGGACAGGCGCGGATGAC	154	
QY	121	TTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCATAGTCCAGCTTCTCT	180	
Db	155	TTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCATAGTCCAGCTTCTCT	214	
QY	181	GGAATTCCTGAAAAG-TCTGCCCTCCCTCCATCTCCCTTCAGGACCA	229	
Db	215	GGAATTCCTGAAAAGCTCTGCCCTCCCTCCATCTCCCTTCAGGACCA	264	
RESULT 3				
BI759796	456 bp mRNA linear EST 27-MAR-2001			
LOCUS	601861290F1 NIH_MGC_77 Homo sapiens cdna clone IMAGE:407059 5',			
DEFINITION	mRNA sequence.			
ACCESSION	BG506690			
VERSION	BG506690.1 GI:13468207			
KEYWORDS	human.			
SOURCE	human.			
ORGANISM	Homo sapiens			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1CM915 row: d column: 24

High quality sequence stop: 401.

Location/Qualifiers

1. .456

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4070759"

/lab_host="NIH-MGC-77"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:

SfII (ggccgctcgcc); Site_2: SfiI (ggccattggcc); 5' and

3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CAGGCGCATATGGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGCGGCGGCACATG-dT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.9

kb (range 0.5-4.0 kb). 12/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH-MGC Library."

BASE COUNT 109 a 137 c 106 g 103 t 1 others

ORIGIN

Query Match 93.9%; Score 215; DB 12; Length 456;

Best Local Similarity 99.6%; Pred. No. 2.8e-51;

Matches 226; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 4 GGGACTCAGTGTCTCTCCATCCAGGAGCGGCGGCGGCTATGGGCTGCGGTCGC 63

Db 2 GGGACTCAGTGTCTCTCCATCCAGGAGCGGCGGCGGCTATGGGCTGCGGTCGC 61

QY 64 CTTTGTCTCTCTCTGACCTCCTTTGGCAGCTCACATGGAACAGCGCGGCTATGACTTT 123

Db 62 CCTTGTCTCTCTCTGACCTCCTTTGGCAGCTCACATGGAACAGCGCGGCTATGACTTT 121

QY 124 GCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCTGGA 183

Db 122 GCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCTGGA 181

QY 184 ATTGCTTGAAAG--TCTGCTCTCTCTCCATCTCCCTTCAGGACCA 229

Db 182 ATTGCTTGAAAGCTCTGCTCTCTCCATCTCCCTTCAGGACCA 228

RESULT 4

BF002050/c

LOCUS 799c11.x1 NCI_CGAP_Col6 422 bp mRNA linear EST 06-OCT-2000

DEFINITION mRNA sequence.

ACCESSION BF002050

VERSION BF002050.1 GI:10702325

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.

, Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov

Seq primer: -40UP from Gibco.

Location/Qualifiers

1. .422

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3314516"

/clone_lib="NCI_CGAP_Col6"

/tissue_type="colon tumor, RER+"

/lab_host="DH10B"

/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; Site_1: Not I; Site_2: Eco RI;

Plasmid DNA from the normalized library NCI_CGAP Col10 was

prepared, and ss circles were made in vitro. Following HAP

purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs

from a pool of 5,000 clones made from the same library

(clonids 1057416-1061255, and 1144584-1145351).

Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 102 a 99 c 130 g 88 t 3 others

ORIGIN

Query Match 93.0%; Score 213; DB 12; Length 422;

Best Local Similarity 97.8%; Pred. No. 1e-50;

Matches 225; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 2 CCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGGCGGCTATGGGCTGCGGCTG 61

Db 422 CCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGGCGGCTATGGGCTGCGGCTG 363

QY 62 CCCCTTGTCTCTCTCTGACCTCCTTTGGCAGCTCACATGGAACAGCGCGGCTATGACT 121

Db 362 CCCCTTGTCTCTCTCTGACCTCCTTTGGCAGCTCACATGGAACAGCGCGGCTATGACT 303

QY 122 TTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCTG 181

Db 302 TTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCTG 243

QY 182 GAATTGCTTGAAAA--GTCTGCTCTCTCTCCATCTCCCTTCAGGACCA 229

Db 242 GAATTGCTTGAAAAAGTWTGCTCTCTCCATCTCCCTTCAGGACCA 193

RESULT 5

BF020029

LOCUS 603037210F1 NIH_MGC_115 895 bp mRNA linear EST 04-OCT-2001

DEFINITION mRNA sequence.

ACCESSION BF020029

VERSION BF020029.1 GI:15931579

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

```
/clone="IMAGE:2408041"
/clone_lib="NCI_CGAP_Lu19"
```


LOCUS	B0664284	522 bp	mRNA	linear	EST 26-OCT-2001
DEFINITION	B0664284 RIKEN full-length enriched, 0 day neonate lung Mus musculus cDNA clone E030032D13 5', mRNA sequence.				
ACCESSION	B0664284				
VERSION	B0664284.1	GI:16498038			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Bases 1 to 522)				
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.				
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-resesc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues. Location/Qualifiers 1. .522 /organism="Mus musculus" /db_xref="taxon:10090" /clone="E030032D13" /clone_lib="RIKEN full-length enriched, 0 day neonate lung" /tissue_type="lung" /dev_stage="0 day neonate" /lab_host="DHI0B" /note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCAACTCGAGTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse				
LOCUS	B0664284	522 bp	mRNA	linear	EST 26-OCT-2001
DEFINITION	B0664284 RIKEN full-length enriched, 0 day neonate lung Mus musculus cDNA clone E030032D13 5', mRNA sequence.				
ACCESSION	B0664284				
VERSION	B0664284.1	GI:16498038			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Bases 1 to 522)				
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.				
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-resesc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues. Location/Qualifiers 1. .522 /organism="Mus musculus" /db_xref="taxon:10090" /clone="E030032D13" /clone_lib="RIKEN full-length enriched, 0 day neonate lung" /tissue_type="lung" /dev_stage="0 day neonate" /lab_host="DHI0B" /note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCAACTCGAGTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse				
LOCUS	B0664284	522 bp	mRNA	linear	EST 26-OCT-2001
DEFINITION	B0664284 RIKEN full-length enriched, 0 day neonate lung Mus musculus cDNA clone E030032D13 5', mRNA sequence.				
ACCESSION	B0664284				
VERSION	B0664284.1	GI:16498038			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Bases 1 to 522)				
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.				
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-resesc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. 				


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/clone="UI-R-C2p-ng-e-02-0-UI"
/clone_lib="UI-R-C2p"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; The UI-R-C2p
library is a substracted library derived from the UI-R-C1
library, which is a substracted library consisted of a
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The substracted library (UI-R-C2p) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3, ESrs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (substracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996)"
791-806, 1996"

BASE COUNT      62 a   77 c   98 g   91 t
ORIGIN

Query Match      27.0%; Score 61.8; DB 9; Length 328;
Best Local Similarity 69.5%; Pred. No. 2.3e-07;
Matches 98; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

QY  90  GCAGCTCACATGGACAGCGCGGTATGACTTTGCAACTGAGCTGAGGAGTCTTTTC 149
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Db  327  GCAGCTCTACTGAGGCGCCAAAGGAGTCTTGGCAAGTAAAGTACGACGAGCATCTC 268
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  150  TGACAAATTCCTTCATGATCCAGCTTCCTGGAAATGCTTGAAAG-TCTGCTCTCTCC 208
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  267  AGGCCAAGACCTCCAGACTCGGCTTTCTGGACATGCTCCAAAAGATCTGCTCTCTCC 208
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  209  TCCATCTCCCTCAGGACCA 229
      ||||| ||| | | | | | | |
Db  207  TCCACCTCTCAGCGGGACCA 187
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RESULT 13
AZ241329/c
LOCUS      AZ241329      506 bp      DNA      linear      GSS 15-JUN-2000
DEFINITION      RPci-23-75C13.TJ RPci-23 Mus musculus genomic clone RPci-23-75C13,
                  DNA sequence.
ACCESSION      AZ241329
VERSION      AZ241329.1 GI:8554520
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 506)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
Mouse BAC End Sequences from Library RPci-23
Unpublished (1999)
Other GSSs: RPci-23-75C13.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

TITLE      Mouse BAC End Sequences from Library RPci-23
JOURNAL
COMMENT
```

```
Clones are derived from the mouse BAC library RPci-23. For BAC
library availability, please contact Pieter de Jong
(pleter@jmg.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 75 row: C column: 13
Seq primer: SP6
Class: BAC ends.
FEATURES
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            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="RPci-23-75C13"
            /clone_lib="RPci-23"
            /sex="Female"
            /lab_host="DH10B"
            /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site.1:
            EcoRI; Site.2: EcoRI; Female C57BL/6J mouse kidney and/or
            brain genomic DNA was isolated and partially digested
            with a combination of EcoRI and EcoRI Methylase. Size
            selected DNA was cloned into the pBACE3.6 vector at the
            EcoRI sites. The ligation products were transformed into
            DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      116 a   145 c   138 g   107 t
ORIGIN

Query Match      19.9%; Score 45.6; DB 17; Length 506;
Best Local Similarity 68.5%; Pred. No. 0.012;
Matches 63; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY  105  CAGGCGCGGTATGACTTTGCAACTGAGCTGAGGAGTCTTTTGTGACAAATTCCTCTC 164
      ||||| ||| | | | | | | | | | | | | | | | | | | | | | | |
Db  403  CAGGCCCAAGGTGACTTTGCGAGGTAAAGCTGACCGAGACTTTTCAGCAGACACCTCCC 344
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  165  ATGAGTCAGAGCTTCCTGGAAATGCTTGAAAG 196
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  343  AGAATCCAGTGTCTGGACATGCTCCAAAAG 312
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
AZ079350/c
LOCUS      AZ079350      633 bp      DNA      linear      GSS 31-MAR-2000
DEFINITION      RPci-23-438H19.TV RPci-23 Mus musculus genomic clone RPci-23-438H19
                  , DNA sequence.
ACCESSION      AZ079350
VERSION      AZ079350.1 GI:7372249
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 633)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
Mouse BAC End Sequences from Library RPci-23
Unpublished (1999)
Other GSSs: RPci-23-438H19.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPci-23. For BAC
library availability, please contact Pieter de Jong
(pleter@jmg.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
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Plate: 438 row: H column: 19

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .633
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-438H19"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methyase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 138 a 191 c 161 g 143 t
ORIGIN

Query Match 19.9%; Score 45.6; DB 17; Length 633;
Best Local Similarity 68.5%; Pred. No. 0.013;
Matches 63; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 105 CAGGCGGGTATGACTTCCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCT 164

Db 403 CAGGGCCAAAGTGACTTGCAGGTAAAGCTGACCGAGACTTTTCAGGACAAAGACCTCCC 344

QY 165 ATGAGTCCAGCTCTCGTAATGCTTGAAAG 196

Db 343 AGAACTCCAGTCTCGACATGCTCCAAAG 312

RESULT 15

EG686317

LOCUS 602638230F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765975 5',
754 bp mRNA linear EST 01-MAY-2001
mRNA sequence.

DEFINITION

EG686317

VERSION

EG686317.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LICM1625 row: 1 column: 08

High quality sequence stop: 750.

Location/Qualifiers

1. .754

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4765975"

/clone_lib="NIH_MGC_48"

/tissue_type="Primary B-cells from tonsils (cell line)"

/lab_host="DH10B (phage-resistant)"

/note="Organ: B-cells; Vector: pOVB7; Site_1: XhoI;

Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA Synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 166 a 206 c 201 g 181 t

ORIGIN

Query Match 15.7%; Score 36; DB 12; Length 754;

Best Local Similarity 64.3%; Pred. No. 7.8; Indels 0; Gaps 0;

Matches 54; Conservative 0; Mismatches 30;

QY 14 TGTCTCTCCATCCAGGAGCGCAGTGGGCTGTGGCTGCCCTTGTCTC 73

Db 249 TGTTCCTCCCTCCAGGATCCCTTTGGTGAGTATGTTTCAGGATGCACCATCACCAC 308

QY 74 CTCTTGACCTCTCTGGCAGTCA 97

Db 309 CTCTAGATACCTTCAGGCAACACA 332

Search completed: May 1, 2003, 05:10:04

Job time : 1150.32 secs

SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,147B
FILING DATE: 29-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 580 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 91..480
US-08-346-147B-7

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Best Local Similarity 57.3%; Pred. No. 0.64;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Qy 35 GCAGTGGCCACTATGGGTCCTGGCGTCCCTTGTCTCTCTGACCCCTCTTGGCAGC 94
Db 128 GGGTGGCCAGGCCGCGTCACTGCTGCGCCCAACATGCGCTTGTCCCGGTCGTGGC 69
Qy 95 TCACATGGAACAGCGCGGATGACTTTGCAACTG 130
Db 68 AGAAATGGTCTCTTGGCGCGCGTGAGATTGCTACAG 33

RESULT 5
US-08-922-936-7/c
Sequence 7, Application US/0822936
Patent No. 6242575
GENERAL INFORMATION:
APPLICANT: Massague, Joan
APPLICANT: Roberts, James M.
APPLICANT: Koff, Andrew
APPLICANT: Polyak, Kornelia
TITLE OF INVENTION: Isolated p27 Protein, Nucleic Acid
TITLE OF INVENTION: Molecules Encoding Same, Methods of Identifying Agents Acting
TITLE OF INVENTION: and Uses of Said Agents
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot, LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,936
FILING DATE: 21-FEBRUARY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-079.05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 580 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 91..480
US-08-822-936-7

Query Match 13.3%; Score 30.4; DB 4; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.64;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 35 GCAGTGGCCACTATGGGTCCTGGCGTCCCTTGTCTCTCTGACCCCTCTTGGCAGC 94
Db 128 GGGTGGCCAGGCCGCGTCACTGCTGCGCCCAACATGCGCTTGTCCCGGTCGTGGC 69
Qy 95 TCACATGGAACAGCGCGGATGACTTTGCAACTG 130
Db 68 AGAAATGGTCTCTTGGCGCGCGTGAGATTGCTACAG 33

RESULT 6
US-08-497-214D-7/c
Sequence 7, Application US/08497214D
Patent No. 6331390
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,214D
FILING DATE: 30-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
COMPUTER READABLE FORM:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA: US 08/227,371
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..480
US-08-497-214D-7

Query Match 13.3%; Score 30.4; DB 4; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.64;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 35 GCAGTGGCCACTATGGGCTGCTGGCTGGCCCTTGTCTCTCTTGACCCCTCTTGGCAGC 94
|| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 128 GCGGTGGCAGGCCGCGTCACTGCTGCCGCCCAACATGCCCTTGTCCCGGTCTGTGSC 69
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QY 95 TCACATGGACAGCGCGGTATGACTTTGCACTG 130
|| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 68 AGAATGGTCTTCGCCGCCGTGAGATTGCTACAG 33
|| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||

RESULT 7
PCT-US95-04636-7/c
; Sequence 7, Application PC/TUS9504636
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related thereto
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
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; APPLICATION NUMBER: PCT/US95/04636
; FILING DATE:
; CLASSIFICATION:
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; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
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; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..480
PCT-US95-04636-7

Query Match 13.3%; Score 30.4; DB 5; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.64;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 35 GCAGTGGCCACTATGGGCTGCTGGCTGGCCCTTGTCTCTCTTGACCCCTCTTGGCAGC 94
|| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 128 GCGGTGGCAGGCCGCGTCACTGCTGCCGCCCAACATGCCCTTGTCCCGGTCTGTGSC 69
|| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
QY 95 TCACATGGACAGCGCGGTATGACTTTGCACTG 130
|| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 68 AGAATGGTCTTCGCCGCCGTGAGATTGCTACAG 33
|| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||

RESULT 8
US-08-928-383B-25
; Sequence 25, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Cocksackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1515 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1095
US-08-928-383B-25
```



```
Query Match 13.3%; Score 30.4; DB 4; Length 1515;
Best Local Similarity 61.2%; Pred. No. 0.99; 31; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 29 AGGAGCGCATGGCCACTATGGGTCTGGGCTGCCCTTGTCTCTCTTGTGACCCCTCTT 88
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 712 ACGATCGCGGCGCGTCATAGGAGCGTGTGGCCCTTGTGTCTCATCGGGCCATCCTC 771
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 89 GGCAGCTCATACATGGACAG 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 772 TTTCTGTCTACAGGAACG 791
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-09-248-571-2
; Sequence 2, Application US/09248571
; Patent No. 6136539
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICHAEL, ASSEFA
; APPLICANT: GENSGH, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5 MUCIN
; FILE REFERENCE: UCSF12/02
; CURRENT APPLICATION NUMBER: US/09/248,571
; EARLIER FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074,398
; EARLIER FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-248-571-2

Query Match 13.1%; Score 30; DB 3; Length 3358;
Best Local Similarity 61.5%; Pred. No. 1.9; 30; Indels 0; Gaps 0;
Matches 48; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 17 CTCCTCCATCCAGGCGCAGTGGCCACTATGGGTCTGGGCTGCCCTTGTCTCTCTC 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 552 CTCATTACAGACGAGCTACACCAAGGTGGAGCGCAGGCTGGGCTTGTCTCTCATG 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 77 TTGACCCCTCTTGGCAGC 94
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 612 TGAACACGATGACAGC 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-09-553-736-2
; Sequence 2, Application US/09553736
; Patent No. 6440672
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, Carol
; APPLICANT: GALLUP, Marianne
; APPLICANT: DAIZONG, Li
; APPLICANT: GEBREMICHAEL, Assefa
; APPLICANT: GENSGH, Erin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-5
; FILE REFERENCE: UCSF-012/03US
; CURRENT APPLICATION NUMBER: US/09/553,736
; CURRENT FILING DATE: 2000-04-20
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: US 09/248,571
; PRIOR FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: US 60/074,398
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

Query Match 13.0%; Score 29.8; DB 2; Length 3509;
Best Local Similarity 51.9%; Pred. No. 2.3; 62; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
```

```
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-553-736-2

Query Match 13.1%; Score 30; DB 4; Length 3358;
Best Local Similarity 61.5%; Pred. No. 1.9; 30; Indels 0; Gaps 0;
Matches 48; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 17 CTCCTCCATCCAGGCGCAGTGGCCACTATGGGTCTGGGCTGCCCTTGTCTCTCTC 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 552 CTCATTACAGACGAGCTACACCAAGGTGGAGCGCAGGCTGGGCTTGTCTCTCATG 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 77 TTGACCCCTCTTGGCAGC 94
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 612 TGAACACGATGACAGC 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-08-817-436A-1
; Sequence 1, Application US/08817436A
; Patent No. 5882880
; GENERAL INFORMATION:
; APPLICANT: Canaan, Dan
; TITLE OF INVENTION: Human Checkpoint Gene and Gene for
; TITLE OF INVENTION: Antisense RNA thereof
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wigman, Cohen, Leitner & Myers
; STREET: 900 17th Street, N.W., Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5 inch, 1.44Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,436A
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12445
; FILING DATE: 11-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Herbert
; REGISTRATION NUMBER: 25,109
; REFERENCE/DOCKET NUMBER: 0744.066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-463-7700
; TELEFAX: 202-463-6915
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3509 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL LINE: ESTABLISHED XERODERMA PIGMENTOSUM GM2096-SV3
; IMMEDIATE SOURCE:
; CLONE: RAP-1 cDNA
US-08-817-436A-1

Query Match 13.0%; Score 29.8; DB 2; Length 3509;
Best Local Similarity 51.9%; Pred. No. 2.3; 62; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
```

```
QY 11 CAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGTCGCCCTTGTG 70
   || || || || || || || || || || || || || || || || || || || || ||
Db 1771 CACGCTCCCTCCATCGGAGAGACCGAGAGAAAGATAACATCTCTATCTCTCTCTGGA 1830
   || || || || || || || || || || || || || || || || || || || || ||
QY 71 CTCCTCTTGACCTCTCTTGGCAGCTCACATGGAACAGCGCGGTATGACTTTGCACTG 130
   || || || || || || || || || || || || || || || || || || || || ||
Db 1831 TACCTCTTGACTTCTCAAGAAACAAAGAAAGAGAGATCTAGTTGGCAGCTT 1890
   || || || || || || || || || || || || || || || || || || || || ||
QY 131 AAGCTGAAG 139
   || || || || ||
Db 1891 AAACGGAG 1899

RESULT 12
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

Query Match 12.9%; Score 29.6; DB 1; Length 7218;
Best Local Similarity 2.3%; Pred. No. 3.7;
Matches 5; Conservative 129; Mismatches 88; Indels 0; Gaps 0;

QY 8 CTTACAGTGTCTCTCCATCCAGGAGCGGAGTGGCCACTATGGGTCTGGGCTGCCCTT 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1219 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 68 GTCTCTCTCTTGACCTCTCTTGGCAGCTCACATGGAACAGCGCGGTATGACTTTGCAA 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1279 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
QY 128 CTGAAGCTGAAGGAGTCTTTTTCGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTG 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1339 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1398
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 188 CTTGAAAAGCTGCGCTCTCTCTCCATCTCCCTTCAGGACCA 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1399 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTACCA 1440

RESULT 13
US-09-219-194-2
; Sequence 2, Application US/09219194
; Patent No. 6410230
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; TITLE OF INVENTION: GLYCERALDEHYDE-3-PHOSPHATE
; DEHYDROGENASE AND NUCLEAR RESTORATION OF CYTOPLASMIC MAL
; STERILITY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SWABEY OGILVY RENAULT
; STREET: 1981 McGill College Ave. - Suite 1600
; CITY: Montreal
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/219,194
; FILING DATE: 23-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/020,553
; FILING DATE: 26-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cote, France
; REGISTRATION NUMBER: 4166
; REFERENCE/DOCKET NUMBER: 1770-152"PCT" F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 514 845-7126
; TELEFAX: 514-288-8389
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-219-194-2

Query Match 12.8%; Score 29.4; DB 4; Length 1091;
Best Local Similarity 63.4%; Pred. No. 1.9;
Matches 45; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 85 CCTTGGCAGCTCACATGGRACAGGCGCGGTATGACTTTTGCACCTGAAGCTGAAGAGTC 144
   || || || || || || || || || || || || || || || || || || || || ||
Db 263 CTGAGGATATCCCATGGGTGAGCGCGGAGCTGACTTTGTTGTTGACTCTACTGGTGC 322
   || || || || || || || || || || || || || || || || || || || || ||
QY 145 TTTTCTGACAA 155
   || || || || || ||
Db 323 TTTCACTGACAA 333

RESULT 14
US-07-709-949-1
; Sequence 1, Application US/07709949
```

; Patent No. 5472858
; GENERAL INFORMATION:
; APPLICANT: Attie, Alan D
; APPLICANT: Gretch, Daniel G
; APPLICANT: Sturley, Stephen L
; APPLICANT: Heckage, Nancy E
; TITLE OF INVENTION: Production of Recombinant Proteins in
; TITLE OF INVENTION: Insect Larvae
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: P.O. Box 2113
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/709,949
; FILING DATE: 19910604
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 9629691801
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 62..1015
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 62..119
; PUBLICATION INFORMATION:
; AUTHORS: McLean, J W
; JOURNAL: Journal of Biological Chemistry
; VOLUME: 259
; PAGES: 6498-6504
; DATE: 1984
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1157

US-07-709-949-1

Query Match 12.7%; Score 29; DB 1; Length 1157;
Best Local Similarity 54.1%; Pred. No. 2.6;
Matches 59; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
Qy 6 GACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTGGGGTGGCCC 65
|| || || || || || || || || || || || || || || || || || || || || ||
Db 626 GAGCGGGCCCTCAGCGCCATCCGCGAGCGCCTGGGGCCCTGTGGTGAACAGGCGCGGTG 685
Qy 66 TTGTCTCTCTCTTGCACCTCTTGGCAGCTCACATGGAACAGGCGCGG 114
|| || || || || || || || || || || || || || || || || || || || || ||
Db 686 CGGGCGGCACTGTGGCTCTCTTGGCGCGCCAGCCGCTACAGGAGCGGG 734

RESULT 15

US-09-056-105-24/c
; Sequence 24, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1316
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-24
Query Match 12.7%; Score 29; DB 4; Length 1316;
Best Local Similarity 57.0%; Pred. No. 2.8;
Matches 53; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
Qy 19 CTCTCATCCAGGAGCGCAGTGGCCACTATGGGTCTGGGGTGGCCCTTGTCTCTCTT 78
|| || || || || || || || || || || || || || || || || || || || || ||
Db 1314 CTTCACGACGCTGGTTCGTGTATATAAGGACTCTTGGTGGCTCTCTCTCTCTCT 1255
Qy 79 GACCCCTCTTGGCAGCTCACATGGAACAGGCGC 111
|| || || || || || || || || || || || || || || || || || || || || ||
Db 1254 CTCTCCAGGATAGAACGATGGAATTAGACC 1222
Search completed: May 1, 2003, 05:13:11
Job time : 49.542 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:55:40 ; Search time 157.34 Seconds

(without alignments)

3277.661 Million cell updates/sec

Title: US-09-092-296-2

Perfect score: 229

Sequence: 1 ACCGGGACTTCAGTGTCTCC.....CCATCTCCTTCAGGGACCA 229

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	218	95.2	422	21	AAZ65087
2	218	95.2	422	22	AAZ65087
3	218	95.2	422	22	AAZ65087
4	218	95.2	422	22	AAZ65087
5	218	95.2	422	22	AAZ65087
6	218	95.2	422	22	AAZ65087
7	114	49.8	624	24	ABK91818
8	109.8	47.9	729	23	AAZ65519
9	34.4	15.0	2923	20	AAZ04326

10	34.4	15.0	3417	22	AAZ94567	Human full-length
11	34	14.8	27082	22	AAZ70447	Human immune/haema
12	32.8	14.3	361	21	AAZ30979	Human secreted pro
13	32.4	14.1	6855	24	ABN83971	Human gene sequenc
14	32	14.0	1128	19	AAV28846	Mouse coxsackievir
15	31.8	13.9	1251	24	ABK09969	Eastern cottonmout
16	31.6	13.8	11749	22	AAZ36066	Human musculoskele
17	31.6	13.8	11749	22	AAZ40590	DNA encoding human
18	31.6	13.8	11749	22	AAZ06478	Human reproductive
19	31.6	13.8	11749	22	AAZ64782	Human immune/haema
20	31.6	13.8	30420	22	AAZ36067	Human musculoskele
21	31.6	13.8	30420	22	AAZ40588	DNA encoding human
22	31.6	13.8	30420	22	AAZ06476	Human reproductive
23	31.2	13.6	2644	23	ABL09867	Human reproductive
24	31.2	13.6	6096	23	ABL09866	Drosophila melanog
25	31.2	13.6	16596	22	AAZ83767	Human immune/haema
26	31.2	13.6	16596	22	AAZ33396	DNA encoding human
27	31	13.5	1243	22	AAZ42525	Partial cDNA seque
28	31	13.5	1498	22	AAZ42526	Nucleotide sequenc
29	30.6	13.4	332	22	AAZ87952	Human digestive sy
30	30.6	13.4	377	22	AAZ89454	Human digestive sy
31	30.6	13.4	705	22	AAH03213	Human cDNA clone (
32	30.6	13.4	2135	22	AAH13650	Human cDNA sequenc
33	30.4	13.3	580	16	AAZ02964	Cell-cycle regulat
34	30.4	13.3	580	20	AAZ80475	Mouse ink-4 protei
35	30.4	13.3	580	20	AAZ13099	Murine cell cycle
36	30.4	13.3	580	24	ABK13272	Mouse cDNA encodin
37	30.4	13.3	1301	19	AAV50430	Mouse coxsackievir
38	30.4	13.3	1318	21	AAZ04640	Arabidopsis thalia
39	30.4	13.3	2387	21	AAZ64276	Human membrane-ass
40	30.4	13.3	3036	23	AAZ92967	DNA encoding novel
41	30.4	13.3	3334	23	AAZ72521	DNA encoding novel
42	30.4	13.3	3874	23	AAZ92969	DNA encoding novel
43	30.4	13.3	3875	23	AAZ72520	DNA encoding novel
44	30.4	13.3	4013	21	AAZ75140	Human ORF695
45	30	13.1	180	24	ABL99631	Toxicologically re

ALIGNMENTS

RESULT 1

AAZ65087
ID AAZ65087 standard; cDNA; 422 BP.

AC AAZ65087;

DT 05-APR-2000 (first entry)

DE Membrane-bound protein PRO1098 encoding cDNA.

DE Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
pharmaceutical; receptor immunoadhesin; gene mapping; ss.

OS Homo sapiens.

PN WO963088-A2.

PD 09-DEC-1999.

PF 02-JUN-1999; 99WO-US12252.

PR 02-JUN-1998; 98US-0087607.

PR 02-JUN-1998; 98US-0087609.

PR 03-JUN-1998; 98US-0087759.

PR 04-JUN-1998; 98US-0088021.

PR 04-JUN-1998; 98US-0088025.

PR 04-JUN-1998; 98US-0088028.

PR 04-JUN-1998; 98US-0088029.

PR 04-JUN-1998; 98US-0088030.

PR 04-JUN-1998; 98US-0088033.

PR 04-JUN-1998; 98US-0088326.

PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090451.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.

PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095516.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.

(GETH) GENENTECH INC.

XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;

XX WPI; 2000-072883/06.

DR P-PSDB; AAY66741.

XX Membrane-bound proteins and related nucleotide sequences -

PS Claim 2; Fig 257; 822pp; English.

XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be

CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.

XX SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 95.2%; Score 218; DB 21; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.1e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 60
DB 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 71
QY 61 GCCCCTTGCTCTCTCTTGACCTCTTGGCAGCTCACATGGAACAGGCGGGTATGAC 120
DB 72 GCCCCTTGCTCTCTCTTGACCTCTTGGCAGCTCACATGGAACAGGCGGGTATGAC 131
QY 121 TTTCGAACCTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGGCTTCT 180
DB 132 TTTCGAACCTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGGCTTCT 191
QY 181 GGAATTGCTTGAAGAAG-TCTGGCTCCTCTCCATCCCTCCATCTCCCTTCAGGGACCA 229
DB 192 GGAATTGCTTGAAGAAGCTCTGCCTCCTCTCCATCTCCCTTCAGGGACCA 241

RESULT 2
AAS46045
ID AAS46045 standard; cDNA; 422 BP.

AC AAS46045;

XX 18-DEC-2001 (first entry)

DT Human DNA encoding PRO polypeptide sequence #121.

DE PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.

XX Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.

PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.

XX (GETH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AI;

PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-602746/68.

DR P-PSDB; AAU29144.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -

XX Claim 2; Fig 241; 774pp; English.

CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.

XX SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 95.2%; Score 218; DB 22; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.1e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 60
DB 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 71
QY 61 GCCCCTTGCTCTCTCTTGACCTCTTGGCAGCTCACATGGAACAGGCGGGTATGAC 120
DB 72 GCCCCTTGCTCTCTCTTGACCTCTTGGCAGCTCACATGGAACAGGCGGGTATGAC 131
QY 121 TTTCGAACCTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGGCTTCT 180
DB 132 TTTCGAACCTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGGCTTCT 191
QY 181 GGAATTGCTTGAAGAAG-TCTGGCTCCTCTCCATCTCCCTTCAGGGACCA 229
DB 192 GGAATTGCTTGAAGAAGCTCTGCCTCCTCTCCATCTCCCTTCAGGGACCA 241

```
RESULT 3
AAF92090
ID   AAF92090 standard; cdNA; 422 BP.
XX
AC   AAF92090;
XX
XX
DT   15-MAY-2001 (first entry)
XX
DE   Human PRO1098 cdNA.
XX
KW   Human; PRO protein; mapping; ss.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
XX
PF   24-AUG-2000; 2000WO-US23328.
XX
PR   01-SEP-1999; 99WO-US20111.
PR   15-SEP-1999; 99WO-US21090.
PR   07-DEC-1999; 99US-0169495.
PR   09-DEC-1999; 99US-0170262.
PR   11-JAN-2000; 2000US-0175481.
PR   18-FEB-2000; 2000WO-US04341.
PR   22-FEB-2000; 2000WO-US04342.
PR   01-MAR-2000; 2000WO-US04414.
PR   03-MAR-2000; 2000WO-US05601.
PR   25-APR-2000; 2000US-0199397.
PR   22-MAY-2000; 2000WO-US14042.
PR   03-JUN-2000; 2000US-0209832.
XX
PA   (GETH ) GENENTECH INC.
XX
XX   Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI   Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
XX   WPI: 2001-183260/18.
XX   P-PSDB; AAB87558.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in
PT   molecular biology, including use as hybridization probes, and in
PT   chromosome and gene mapping.
XX
XX   Claim 2; Fig 65; 278pp; English.
XX
CC   The present sequence is the coding sequence for a human PRO polypeptide
CC   (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC   antagonists or anti-PRO antibodies are useful for preparation of a
CC   medicament useful in the treatment of a condition which is responsive to
CC   the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC   protein may also be employed as molecular weight markers for protein
CC   electrophoresis. The PRO coding sequence has applications in molecular
CC   biology, including use as hybridisation probes, and in chromosome and
CC   gene mapping.
XX
SQ   Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;
Query Match          95.2%; Score 218; DB 22; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.1e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY   1 ACCGGGACTTCAGTCTCTCCATCCCGAGGCGGACGTGGCCACTATGGGTCGTGGGCT 60
Db   |||||||
QY   12 ACCGGGACTTCAGTGTCTCTCCATCCCGAGGCGGACGTGGGTCGTGGGCT 71
Db   |||||||
QY   61 GCCCCTTGTCCTCTTGCACCTCTTGGCAGCTCACATGGAACAGGCGCGGTATGAC 120
Db   |||||||
QY   72 GCCCCTTGTCCTCTTGCACCTCTTGGCAGCTCACATGGAACAGGCGCGGTATGAC 131
Db   |||||||

QY   121 TTGCACTGAAGCTGAAGAGCTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 180
Db   |||||||
QY   132 TTGCACTGAAGCTGAAGAGCTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 191
Db   |||||||
QY   181 GGAATTGCTGAAAAG-TCTGCCTCCCTCCCATCTCCCTTCAGGACCA 229
Db   |||||||
QY   192 GGAATTGCTGAAAAGCTCTGCCTCCCTCCCATCTCCCTTCAGGACCA 241
Db   |||||||

RESULT 4
AAF44233
ID   AAF44233 standard; cdNA; 422 BP.
XX
AC   AAF44233;
XX
XX
DT   02-APR-2001 (first entry)
XX
DE   Human PRO1098 (UNQ541) nucleotide sequence SEQ ID NO:362.
XX
XX
KW   Human; secreted and transmembrane protein; PRO; cytotstatic;
KW   cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW   diagnostic assay; ss.
XX
OS   Homo sapiens.
XX
XX   WO200073454-A1.
XX
XX   07-DEC-2000.
XX
XX   30-MAR-2000; 2000WO-US08439.
XX
XX   02-JUN-1999; 99WO-US12252.
XX   23-JUN-1999; 99US-0141037.
XX   07-JUL-1999; 99US-0143048.
XX   20-JUL-1999; 99US-0144758.
XX   26-JUL-1999; 99US-0145698.
XX   28-JUL-1999; 99US-0146222.
XX   17-AUG-1999; 99US-0149386.
XX   15-SEP-1999; 99WO-US21090.
XX   15-SEP-1999; 99WO-US21547.
XX   08-OCT-1999; 99US-0158663.
XX   30-NOV-1999; 99WO-US28313.
XX   01-DEC-1999; 99WO-US28301.
XX   16-DEC-1999; 99WO-US30095.
XX   20-DEC-1999; 99WO-US30911.
XX   05-JAN-2000; 2000WO-US00219.
XX   06-JAN-2000; 2000WO-US00376.
XX   11-FEB-2000; 2000WO-US03565.
XX   18-FEB-2000; 2000WO-US04341.
XX   22-FEB-2000; 2000WO-US04414.
XX   24-FEB-2000; 2000WO-US04914.
XX   24-FEB-2000; 2000WO-US05004.
XX   02-MAR-2000; 2000WO-US05841.
XX   15-MAR-2000; 2000WO-US06884.
XX   20-MAR-2000; 2000WO-US07377.
XX
XX   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI   Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI   Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI   Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI   Zhang Z;
XX
XX   WPI: 2001-032160/04.
XX   P-PSDB; AAB65284.
XX
PT   PRO polynucleotides used to produce polypeptides used to target
PT   bioactive molecules such as toxins, radiolabels or antibodies, to
PT   specific cells, to cause targeted cell death -
XX
PS   Claim 2; Fig 257; 935pp; English.
```



```

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 75..311
XX FT /*tag= a
XX FT /note= "cDNA comprising the coding region (minus
XX the stop codon) is claimed (Claim 3)"
XX
XX W09855508-A2.
XX
XX 10-DEC-1998.
XX
XX 03-JUN-1998; 98WO-JP02445.
XX
XX 03-JUN-1997; 97JP-0144948.
XX
XX (PROT-) PROTEGENE INC.
XX (SAGA ) SAGAMI CHEM RES CENTRE.
XX
XX Kato S, Sekine S, Yamaguchi T;
XX
XX WPI; 1999-045730/04.
XX P-FSDB; AAW88498.
XX
XX New human proteins containing transmembrane domains and their
XX encoding sequences - useful in the preparation of antibodies and
XX large-scale protein production, gene diagnosis, and gene therapy
XX
XX Claim 4; Page 135; 178pp; English.
XX
XX This is the nucleotide sequence of cDNA clone HP10408, which
XX includes a coding region (also claimed) for a novel human
XX transmembrane protein (see AAW88498). The clone was isolated from a
XX stomach cancer cDNA library using a signal sequence detection
XX method, and by protein synthesis by in vitro translation. The
XX encoded protein has a putative signal sequence and a putative
XX internal transmembrane domain. The invention provides nucleotide
XX sequences (see AAW84359-76) coding for 18 transmembrane proteins
XX (see AAW88491-508), vectors containing such polynucleotides, and
XX eukaryotic cells containing the vectors. The proteins can be
XX used as antigens or as compositions in the preparation of
XX antibodies against the proteins. The polynucleotides can be used
XX as probes for gene diagnosis, and as gene sources for gene therapy
XX and large-scale production of proteins encoded by the cDNA. The
XX host cells are used for the detection of ligands corresponding to
XX the expressed proteins, and the screening of low mol.wt. medicines.
XX
XX Sequence 439 BP; 89 A; 137 C; 109 G; 104 T; 0 other;
XX
XX Query Match 95.2%; Score 218; DB 20; Length 439;
XX Best Local Similarity 99.6%; Pred. No. 2.le-60;
XX Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX QY 1 ACCGGGACATTCAGTGTCTCTCCATCCAGAGGCGCAGTGCCACATATGGGGTCTGGGCT 60
XX |
XX Db 29 ACCGGGACATTCAGTGTCTCTCCATCCAGAGGCGCAGTGCCACATATGGGGTCTGGGCT 88
XX |
XX QY 61 GCCCCTTGCTCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACAGGCGGGGTATGAC 120
XX |
XX Db 89 GCCCCTTGCTCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACAGGCGGGGTATGAC 148
XX |
XX QY 121 TTTCGAAGTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 180
XX |
XX Db 149 TTTCGAAGTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 208
XX |
XX QY 181 GGAATTCCTGGAAGG-TCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 229
XX |
XX Db 209 GGAATTCCTGGAAGGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 258
XX |
XX
XX RESULT 7
XX ABK81818

```

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ID ABK81818 standard; DNA; 624 BP.
XX
XX AC ABK81818;
XX
XX DT 13-AUG-2002 (first entry)
XX
XX DE DNA representing lung specific gene #4.
XX
XX KW Lung specific gene; gene therapy; vaccine; lung cancer;
XX KW cancer staging; cancer monitoring; cancer diagnosis;
XX KW imaging lung cancer; metastases; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN W0200218576-A2.
XX
XX PD 07-MAR-2002.
XX
XX PF 27-AUG-2001; 2001WO-US26684.
XX
XX PR 28-AUG-2000; 2000US-228378P.
XX
XX PA (DIAD-) DIADEXUS INC.
XX
XX PI Chen S, Macina RA, Sun Y, Recipon H;
XX
XX DR WPI; 2002-434904/46.
XX
XX PT New lung specific genes and their encoded proteins, useful in gene
XX PT therapy or as a vaccine for treating lung cancer, as well as for
XX PT measuring metastases of lung cancer, or staging, monitoring, diagnosing
XX PT or imaging lung cancer -
XX
XX PS Claim 1; Page 161; 206pp; English.
XX
XX CC The invention describes a new lung specific gene and it's variants. The
XX CC lung specific gene proteins and genes are useful in gene therapy or as a
XX CC vaccine for treating lung cancer. Lung specific genes are also useful for
XX CC staging, monitoring, diagnosing or imaging lung cancer, as well as for
XX CC measuring metastases of lung cancer. This sequence represents a lung
XX CC specific gene described in the invention.
XX
XX SQ Sequence 624 BP; 129 A; 175 C; 182 G; 138 T; 0 other;
XX
XX Query Match 49.8%; Score 114; DB 24; Length 624;
XX Best Local Similarity 99.2%; Pred. No. 9.2e-27;
XX Matches 125; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX QY 105 CAGGGCCGGGTATGACTTTCGCACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCT 164
XX |
XX Db 314 CAGGGCCGGGTATGACTTTCGCACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCT 373
XX |
XX QY 165 ATGAGTCCAGCTTCTCGAATTTGAAAAG-TCTGCCCTCCTCCTCCATCTCCCTTCAG 223
XX |
XX Db 374 ATGAGTCCAGCTTCTCGAATTTGAAAAGTCTGCCCTCCTCCTCCATCTCCCTTCAG 433
XX |
XX QY 224 GGACCA 229
XX |
XX Db 434 GGACCA 439
XX |
XX
XX RESULT 8
XX AAS65519
XX ID AAS65519 standard; cDNA; 729 BP.
XX
XX AC AAS65519;
XX
XX DT 13-FEB-2002 (first entry)
XX
XX DE DNA encoding novel human diagnostic protein #1323.
XX
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

```

XX Homo sapiens.
 OS WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 DR P-PSDB; ABG01332.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 1; SEQ ID NO 1323; 103pp; English.
 PS The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: the sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 729 BP; 187 A; 169 C; 152 G; 146 T; 75 other;
 Query Match 47.9%; Score 109.8; DB 23; Length 729;
 Best Local Similarity 98.2%; Pred. No. 2.2e-25;
 Matches 111; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 30 GGAGGCGAGTGGGCGACTATGGGCTGGGCTGCCCTTCTCTCTTGACCTCCTTTG 89
 Db 8 GGAGGCGAGGCGACTATGGGCTGGGCTGCCCTTCTCTCTTGACCTCCTTTG 67
 Oy 90 GCAGTTCACATGGGAACAGCGCGGTATGACTTTGCACTGAAGCTGAAGGAG 142
 Db 68 GCAGTTCACATGGGAACAGCGCGGTATGACTTTGCACTGAAGCTGAAGGAG 120
 RESULT 9
 AAX04326
 ID AAX04326 standard; DNA; 2923 BP.
 XX AC AAX04326;
 XX 13-APR-1999 (first entry)
 DT Human secreted protein gene 16 clone HSHBQ68.
 DE
 XX

KW Human: secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX Homo sapiens.
 OS WO9856804-A1.
 PN 17-DEC-1998.
 XX 11-JUN-1998; 98WO-US12125.
 PF 02-OCT-1997; 97US-0061060.
 PR 13-JUN-1997; 97US-0049547.
 PR 13-JUN-1997; 97US-0049548.
 PR 13-JUN-1997; 97US-0049549.
 PR 13-JUN-1997; 97US-0049550.
 PR 13-JUN-1997; 97US-0049606.
 PR 13-JUN-1997; 97US-0049607.
 PR 13-JUN-1997; 97US-0049608.
 PR 13-JUN-1997; 97US-0049609.
 PR 13-JUN-1997; 97US-0049610.
 PR 13-JUN-1997; 97US-0050566.
 PR 13-JUN-1997; 97US-0050901.
 PR 08-JUL-1997; 97US-0052989.
 PR 18-AUG-1997; 97US-0051919.
 PR 12-SEP-1997; 97US-0058665.
 PR 12-SEP-1997; 97US-0058668.
 PR 12-SEP-1997; 97US-0058669.
 PR 12-SEP-1997; 97US-0058750.
 PR 12-SEP-1997; 97US-0058971.
 PR 12-SEP-1997; 97US-0058972.
 PR 02-OCT-1997; 97US-0060834.
 PR 02-OCT-1997; 97US-0060841.
 PR 02-OCT-1997; 97US-0060844.
 PR 02-OCT-1997; 97US-0060865.
 PR 02-OCT-1997; 97US-0061059.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Brewer LA, Ebner R, Ferlie AM, Feng P, Greene JM, Lafleur DW;
 PI Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
 PI Yu GL;
 XX WPI; 1999-080881/07.
 DR P-PSDB; AAW78141.
 XX New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX Claim 1; Page 180-182; 380pp; English.
 PS This sequence represents a nucleic acid molecule which encodes a
 CC secreted human protein. The gene number, and the clone it is derived
 CC from, are detailed in the descriptor line. The gene can be used to
 CC generate fusion proteins by linking to the gene to a human immunoglobulin
 CC Fc portion (e.g. AAX04302) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 86 novel genes and their fragments (nucleic
 CC acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in

PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-02311242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234397.
PR 25-SEP-2000; 2000US-0234398.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246612.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.

PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-483426/52.
DR
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Disclosure; SEQ ID NO 25259; 3071pp + Sequence Listing; English.
PS
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 27082 BP; 5963 A; 7786 C; 7711 G; 5622 T; 0 other;
Query Match 14.8%; Score 34; DB 22; Length 27082;
Best Local Similarity 54.9%; Pred. No. 2.7;
Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
Qy 15 GTCTCTCCATCCAGGAGCGAGTGGCTACTATGGGGTCTGGGGTCCCTTCTCTCC 74
Db 13016 GGCTACTCTAGGATAAGCCCGCTCCCTCATCTCCCTGACGTCCTGACCCCA 13075
Qy 75 TCTTGACCTCTCTTGGCAGCTCACATGGAACAGGGCGGGTATGACTTTGCACTGAAGC 134
Db 13076 TCTACTCTCTCTGGGACTTCTCAGCCACCAGGGCTGGGCTTTCACATGCAAGG 13135
Qy 135 TG 136
Db 13136 TG 13137
RESULT 12

KW pancreatic infection; acute pancreatitis; gastrointestinal tract;
KW diabetes mellitus; ss.
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..1128
FT /tag= a
FT /product= "coxsackievirus and adenovirus receptor"
FT /transl_except= (pos:1096..1098,aa:Xaa)
FT /note= "Xaa= a stop codon, the sequence is shown as
continuing but gets unclear"
XX
FN WO9811221-A2.
XX
XX 19-MAR-1998.
PD
XX
XX 12-SEP-1997; 97WO-US16189.
XX
XX 13-SEP-1996; 96US-0026100.
PR
XX (DAND) DANA FARBEN CANCER INST INC.
XX
XX Bergelson JM, Finberg RW, Horowitz MS;
XX WPI; 1998-207384/18.
XX P-PSDB; AAW57213.
DR
XX
XX DNA encoding coxsackie virus and adenovirus receptor - useful for
PT modulation of e.g. cardiac, pancreatic or gastrointestinal infection
XX
XX Disclosure; Fig 14; 104pp; English.
XX
XX The present sequence encodes mouse coxsackievirus and adenovirus
CC receptor (CAR). The present invention also describes: (1) a method for
CC modulating CAR expression comprising contacting the cell with an agent
CC which modulates CAR protein activity or CAR nucleic acid expression,
CC such that a cell associated activity is altered relative to a cell
CC associated activity of the cell in the absence of the agent; and (2) a
CC method for detecting the presence of CAR in a biological sample
CC comprising contacting a biological sample with an agent capable of
CC detecting CAR protein or mRNA such that the presence of CAR is detected.
CC Modulation of CAR is useful for treatment of cardiac infection, e.g.
CC myocarditis, pericarditis or dilated cardiomyopathy, or infection of the
CC central nervous system, e.g. a non-specific febrile illness or
CC meningoencephalitis, or pancreatic infection, e.g. acute pancreatitis,
CC or infection of the respiratory or gastrointestinal tract or childhood
CC onset diabetes mellitus. Probes derived from CAR nucleic acids are
CC useful for hybridisation assays, and antibodies raised against CAR
CC protein are useful for blocking CAR expression. Cell-free assays which
CC include combining CAR protein and a candidate/test compound are useful
CC in screening for drugs which interact with CAR protein.
XX
SQ Sequence 1128 BP; 297 A; 286 C; 288 G; 257 T; 0 other;
Query Match 14.0%; Score 32; DB 19; Length 1128;
Best Local Similarity 62.5%; Pred. No. 3.4;
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 29 AGGAGCGAGTGGCCACTGTGGGCTGGCCCTTGTCTCTCTTGTGACCCCTCTT 88
Db 712 ACGATCGGGCGCGTCGTAGGACGCTGTGGCCCTTGTCTCTCTGCGGCATCCCTC 771
QY 89 GCGAGCTCACATGAACAGG 108
Db 772 TTCTGCTGTACAGGAAGG 791
RESULT 15
ABK09969
ID ABK09969 standard; cDNA; 1251 BP.
XX
AC ABK09969;

XX 21-MAY-2002 (first entry)
DT
XX Eastern cottonmouth snake zsnk1 gene sequence.
DE
XX
KW Eastern cottonmouth snake; zsnk1; gene; snake venom; blood pressure;
KW vascular permeability; heparin binding; cell proliferation; mitogenesis;
KW hypotensive; cytostatic; antirheumatic; antiarthritic; antidiabetic;
KW vasotropic; antiarteriosclerotic; vulnerary; antitumor; hepatotropic;
KW antinflammatory; vaccine; gene therapy; angiogenesis regulator;
KW neurite outgrowth; organ development; organ regeneration; cancer; ss.
XX
XX Agkistrodon piscivorus piscivorus.
XX
XX Key Location/Qualifiers
FH CDS 201..638
FT /tag= a
FT /product= "Eastern cottonmouth snake zsnk1 protein"
FT misc_feature 201..435
FT /tag= b
FT /note= "Used to make snake venom polypeptide.
Specifically claimed in claim 2d"
FT
FT sig_peptide 201..263
FT /tag= c
FT sig_peptide 201..254
FT /tag= d
FT /note= "Alternative signal peptide #1"
FT sig_peptide 201..248
FT /tag= e
FT /note= "Alternative signal peptide #2"
FT misc_feature 249..435
FT /tag= f
FT /note= "Used to make snake venom polypeptide.
Specifically claimed in claim 2c"
FT
FT mat_peptide 249..635
FT /tag= g
FT /note= "Alternative mature peptide #2"
FT mat_peptide 255..635
FT /tag= h
FT /note= "Alternative mature peptide #1"
FT misc_feature 255..435
FT /tag= i
FT /note= "Used to make snake venom polypeptide.
Specifically claimed in claim 2b"
FT
FT mat_peptide 264..635
FT /tag= j
FT misc_feature 264..435
FT /tag= k
FT /note= "Used to make snake venom polypeptide.
Specifically claimed in claim 2a"
XX
XX WO200212334-A2.
XX
XX 14-FEB-2002.
XX
XX 07-AUG-2001; 2001WO-US24999.
XX
XX 07-AUG-2000; 2000US-223164P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO;
XX
XX WPI; 2002-217178/27.
DR P-PSDB; AAU76683.
XX
XX New snake venom zsnk1 polypeptide and polynucleotide, useful for
PT decreasing blood pressure, causing vascular permeability, binding
PT heparin and inducing proliferation or mitogenesis in cells -
XX
XX Claim 2; Page 98-99; 103pp; English.
XX
XX The present invention relates to a new snake venom zsnk1 polypeptide
CC

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:59:25 ; Search time 748.794 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

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Maximum Match 100%
Listing first 45 summaries

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8: gb_pl:*
9: gb_pr:*
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11: gb_sts:*
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14: gb_vi:*
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27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	218	95.2	422	6	AX092334	AX092334 Sequence
2	218	95.2	422	6	AX376174	AX376174 Sequence
3	218	95.2	422	6	AX403475	AX403475 Sequence
4	216.4	94.5	484	9	AY102070	AY102070 Homo sapi
5	114	49.8	624	6	AX472955	AX472955 Sequence
6	109.4	47.8	47323	9	AC005937	AC005937 Homo sapi
c 7	109.4	47.8	84474	9	AL662854	AL662854 Human DNA
8	109.4	47.8	104154	2	AL773541	AL773541 Homo sapi
c 9	109.4	47.8	156272	9	AL669830	AL669830 Human DNA
10	109.4	47.8	178688	2	AL713893	AL713893 Homo sapi
11	109.4	47.8	192650	9	AB023048	AB023048 Homo sapi
12	109.4	47.8	200000	9	AF000511	AF000511 Homo sapi
c 13	66	28.8	349980	6	AX344553	AX344553 Sequence
c 14	66	28.8	349980	6	AX344554	AX344554 Sequence
15	62.2	27.2	349980	6	AX344571	AX344571 Sequence
c 16	45.6	19.9	175345	2	AC022301	AC022301 Mus muscu
17	44.8	19.6	132977	2	RN510D20	AL603723 Rattus no
18	44.8	19.6	337832	2	AC099175	AC099175 Rattus no
c 19	38.2	16.7	130742	2	AF005653	AF005653 Oryza sat
c 20	37.8	16.5	185154	2	AC127110	AC127110 Rattus no
21	36	15.7	155406	2	AC105514	AC105514 Rattus no
22	35.8	15.6	196840	9	AC104435	AC104435 Homo sapi
c 23	35.8	15.6	203773	9	AC097369	AC097369 Homo sapi
24	35.4	15.5	146399	9	AC025835	AC025835 Homo sapi
c 25	34.8	15.2	176994	2	AC118783	AC118783 Rattus no
26	34.8	15.2	188082	2	AC121784	AC121784 Mus muscu
27	34.8	15.2	197344	2	AC102613	AC102613 Mus muscu
28	34.8	15.2	243644	2	AC097608	AC097608 Rattus no
c 29	34.4	15.0	2032	9	AK025566	AK025566 Homo sapi
30	34.4	15.0	77322	9	HSDJ144C9	AL096774 Human DNA
31	34.4	15.0	141272	9	AF001976	AF001976 Homo sapi
c 32	34.4	15.0	154937	2	AP002382	AP002382 Homo sapi
c 33	34.4	15.0	183887	9	AC017033	AC017033 Homo sapi
c 34	34.4	15.0	187027	2	AC019078	AC019078 Homo sapi
c 35	34.4	15.0	202995	2	AC019134	AC019134 Homo sapi
c 36	34.4	15.0	333841	2	AL161641	AL161641 Homo sapi
37	34.2	14.9	188406	2	AC079560	AC079560 Mus muscu
c 38	34.2	14.9	203155	2	AC079473	AC079473 Mus muscu
39	34.2	14.9	292172	2	AC125207	AC125207 Mus muscu
40	34	14.8	1801	8	OSU25430	U25430 Oryza sativ
41	34	14.8	3753	8	AF245483	AF245483 Oryza sat
42	34	14.8	36676	9	HSJ858B16	AL096768 Human DNA
43	34	14.8	77691	9	AC120118	AC120118 Homo sapi
44	34	14.8	100521	9	AC119397	AC119397 Homo sapi
45	34	14.8	149610	8	AF003244	AF003244 Oryza sat

ALIGNMENTS

RESULT 1
AX092334
LOCUS AX092334
DEFINITION Sequence 65 from Patent WO0116318.
ACCESSION AX092334
VERSION AX092334.1 GI:13444481
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 422)
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 65 08-MAR-2001;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
 source
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN

Query Match 95.2%; Score 218; DB 6; Length 422;
Best Local Similarity 99.6%; Pred. No. 4.9e-58;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 60
 |||||
Db 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 71
 |||||
QY 61 GCCCTGTGCTCCCTTTGACCCCTCTTGGAGCTCATGGAACAGCGCGGTATGAC 120
 |||||
Db 72 GCCCTGTGCTCCCTTTGACCCCTCTTGGAGCTCATGGAACAGCGCGGTATGAC 131
 |||||
QY 121 TTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 180
 |||||
Db 132 TTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 191
 |||||
QY 181 GGAATTGCTTGAAGAAG-TCTGCTCTCTCTCCATCTCCTTCAGGAGCA 229
 |||||
Db 192 GGAATTGCTTGAAGAAGCTGCTCTCTCTCCATCTCCTTCAGGAGCA 241
 |||||

RESULT 2
AX376174
LOCUS AX376174 422 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 241 from Patent WO0168848.
ACCESSION AX376174
VERSION AX376174.1 GI:19170479
KEYWORDS human.
SOURCE Homo sapiens
 Location/Qualifiers
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
 Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
 Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 241 20-SEP-2001;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
 source
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN

Query Match 95.2%; Score 218; DB 6; Length 422;
Best Local Similarity 99.6%; Pred. No. 4.9e-58;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 60
 |||||
Db 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 71
 |||||
QY 61 GCCCTGTGCTCCCTTTGACCCCTCTTGGAGCTCATGGAACAGCGCGGTATGAC 120
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Db 72 GCCCTGTGCTCCCTTTGACCCCTCTTGGAGCTCATGGAACAGCGCGGTATGAC 131
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QY 121 TTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 180
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Db 132 TTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 191
 |||||

QY 181 GGAATTGCTTGAAGAAG-TCTGCTCTCTCTCCATCTCCTTCAGGAGCA 229
 |||||
Db 192 GGAATTGCTTGAAGAAGCTGCTCTCTCTCCATCTCCTTCAGGAGCA 241
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RESULT 3
AX403475
LOCUS AX403475 422 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 362 from Patent WO0073454.
ACCESSION AX403475
VERSION AX403475.1 GI:21436973
KEYWORDS human.
SOURCE Homo sapiens
 Location/Qualifiers
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,
 Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,
 Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,
 Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
 Williams, P., Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 362 07-DEC-2000;
Genentech Inc. (US)
FEATURES Location/Qualifiers
 source
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN

Query Match 95.2%; Score 218; DB 6; Length 422;
Best Local Similarity 99.6%; Pred. No. 4.9e-58;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 60
 |||||
Db 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 71
 |||||
QY 61 GCCCTGTGCTCCCTTTGACCCCTCTTGGAGCTCATGGAACAGCGCGGTATGAC 120
 |||||
Db 72 GCCCTGTGCTCCCTTTGACCCCTCTTGGAGCTCATGGAACAGCGCGGTATGAC 131
 |||||
QY 121 TTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 180
 |||||
Db 132 TTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 191
 |||||
QY 181 GGAATTGCTTGAAGAAG-TCTGCTCTCTCTCCATCTCCTTCAGGAGCA 229
 |||||
Db 192 GGAATTGCTTGAAGAAGCTGCTCTCTCTCCATCTCCTTCAGGAGCA 241
 |||||

RESULT 4
AY102070
LOCUS AY102070 484 bp mRNA linear PRI 18-JUN-2002
DEFINITION Homo sapiens surfactant associated protein G mRNA, partial
sequence.
ACCESSION AY102070
VERSION AY102070.1 GI:21464498
KEYWORDS human.
SOURCE Homo sapiens
 Location/Qualifiers
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 484)
 Walker, M.G. and Spiro, P.
TITLE Genes co-expressed with pulmonary surfactants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 484)
 Walker, M.G. and Spiro, P.

TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Incyte Genomics, 1475 Flamingo Way,
Sunnyvale, CA 94087-3405, USA
FEATURES
source Location/Qualifiers
1..484
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="236582"
<1..>484
/gene="surfactant associated protein G"
/note="SFTPG"

BASE COUNT 124 a 149 c 110 g 101 t
ORIGIN

Query Match 94.5%; Score 216.4; DB 9; Length 484;
Best Local Similarity 99.1%; Pred. No. 1.6e-57;
Matches 228; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 ACCGGACTTCAGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTGGCT 60
|||||
Db 9 ACCGGACTTCAGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTGGCT 68
|||||
QY 61 GCCCCTTGCTCTCTGACCTCTGCGAGCTCATGGAACAGGCGCGGTATGAC 120
|||||
Db 69 GCCCCTTGCTCTCTGACCTCTGCGAGCTCATGGAACAGGCGCGGTATGAC 128
|||||
QY 121 TTGTGAACCTGAAGCTGAGGAGTCTTTCTGACAAATCTCTGATGATCCAGCTTCCT 180
|||||
Db 129 TTGTGAACCTGAAGCTGAGGAGTCTTTCTGACAAATCTCTGATGATCCAGCTTCCT 188
|||||
QY 181 GGAATGCTTGAAGAAG-TCTGCGCTCTCTCCATCTCCCTTCAGGACCA 229
|||||
Db 189 GGAATGCTTGAAGAAGCTCTGCGCTCTCCATCTCCCTTCAGGACCA 238
|||||

RESULT 5
AX472955
LOCUS AX472955 624 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 4 from Patent WO0218576.
ACCESSION AX472955
VERSION AX472955.1 GI:22207742
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Chen, S.Y., Macina, R.A., Sun, Y. and Recipon, H.
TITLE Compositions and methods relating to lung specific genes
JOURNAL Patent: WO 0218576-A 4 07-MAR-2002;
Diadexus, Inc. (US)
FEATURES
source Location/Qualifiers
1..624
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 129 a 175 c 182 g 138 t
ORIGIN

Query Match 49.8%; Score 114; DB 6; Length 624;
Best Local Similarity 99.2%; Pred. No. 4.4e-25;
Matches 125; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 105 CAGGCGGGATGACATTCGACCTGAAGAGTCTTTCTGACAAATTCCTTCCT 164
|||||
Db 314 CAGGCGGGATGACATTCGACCTGAAGAGTCTTTCTGACAAATTCCTTCCT 373
|||||
QY 165 ATGAGTCCAGCTTCTCGAATTCGTTGAAAG-TCTGCCCTCTCTCCATCTCCCTTCAG 223
|||||
Db 374 ATGAGTCCAGCTTCTCGAATTCGTTGAAAGTCTGCCCTCTCTCCATCTCCCTTCAG 433
|||||
QY 224 GGACCA 229
|||||
Db 434 GGACCA 439
|||||

RESULT 6
AC005937
LOCUS AC005937 47323 bp DNA linear PRI 05-NOV-1998
DEFINITION Homo sapiens clone UWGC:370M23.002 from 6p21, complete sequence.
AC005937
ACCESSION AC005937
VERSION AC005937.1 GI:3845393
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (Bases 1 to 47323)
AUTHORS Janer, M., Guillaudoux, T., Vu, Q., Kutayavin, T., Harter, H. and
Geraghty, D.E.
TITLE Large scale sequence analysis of the human MHC class I region
JOURNAL Unpublished (1998)
REMARK Fred Hutchinson Cancer Research Center
The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
2 (Bases 1 to 47323)
Geraghty, D.E. and Olson, M.V.
Direct Submission
Submitted (05-NOV-1998) Human Genome Center, University of
Washington, Box 352145, Seattle, WA 98195, USA
University of Washington Human Genome Center
Box 352145 Seattle, WA 98195
Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
Overlapping Sequences:
5': UWGC:370M23.013 (Genbank Accession: AC005530)
3': UWGC:y67c112 (Genbank Accession: AC004211)

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

Double stranded (DS) coverage: 75.5%
DS or two chemistry coverage: 98.9%
Single stranded regions: 3

Sequence Validation:
This sequence has been validated by Multiple Complete Digest
Mapping. Comparison of the experimentally derived map digest
fragments with sequence-predicted fragments is given below.
Small fragments below a variable cutoff (approximately 400-600bp)
are not mapped and hence do not appear in the table. There are no
significant remaining discrepancies between the experimental and
predicted values. Uniquely ordered fragment groups are separated
by dashed lines.
BglII HindIII
Map Seq Map Seq Map Seq

1069.11 1050.00 889.55 866.00 30541.40 30653.00

20320.67 20855.00 1050.18 1015.00 3279.08 3231.00

2171.50 2147.00 7268.78 7196.00

2560.20 2531.00 10085.80 9992.00

4335.42 4269.00 11212.78 11131.00

2698.62 2628.00

1927.50 1887.00


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Best Local Similarity 95.0%; Pred. No. 1.7e-23;
Matches 113; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 60
|||||
Db 56560 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 56501
|||||

QY 61 GCCCCTTGCTCCTCTTGACCCCTCTTGCCAGCTCACAATGGAACAGGCGCGGTATGA 119
|||||
Db 56500 GCCCCTTGCTCCTCTTGACCCCTCTTGCCAGCTCACAATGGAACAGGCTGAGGCTAGA 56442
|||||

RESULT 8
AL773541
LOCUS
DEFINITION
Homo sapiens chromosome 6 clone XXbac-11J22, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
ACCESSION
AL773541
VERSION
AL773541.4 GI:22204637
KEYWORDS
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Almeida, J.
Direct Submission
Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 11, 2002 this sequence version replaced gi:21621737.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BOB11J22
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 104135 bases at least Q40
Consensus quality: 104142 bases at least Q30
Consensus quality: 104145 bases at least Q20
Insert size: 110727; 1.1% error; agarose-fp
Quality coverage: 19.52x in Q20 bases; sum-of-contigs Quality
coverage: 18.64x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
1. .104154
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-11J22"
/clone_lib="DNA-arts-BAC.1-QBL.1"
misc_feature
1. .104154
/note="assembly_fragment:00090"
BASE COUNT
26560 a 25418 c 26093 g 26083 t
ORIGIN

Query Match 47.8%; Score 109.4; DB 2; Length 104154;
Best Local Similarity 95.0%; Pred. No. 1.7e-23;
Matches 113; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 60
|||||
Db 67502 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 67561
|||||

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```

QY 61 GCCCCTTGCTCCTCTTGACCCCTCTTGCCAGCTCACAATGGAACAGGCGCGGTATGA 119
|||||
Db 67562 GCCCCTTGCTCCTCTTGACCCCTCTTGCCAGCTCACAATGGAACAGGCTGAGGCTAGA 67620
|||||

RESULT 9
AL669830/c
LOCUS
DEFINITION
Human DNA sequence from clone XXbac-118E17 on Chromosome 6,
complete sequence.
ACCESSION
AL669830
VERSION
AL669830.9 GI:20135762
KEYWORDS
HTG.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Johnson, C.
Direct Submission
Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 10, 2002 this sequence version replaced gi:20067510.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em.; EMBL; SW.;
SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep/XXbac-118E17 is
from a CHORI-501 human bac - PGF cell line library VECTOR:
PTARBAC2.1
This sequence was generated from part of bacterial clone contigs
constructed by the MHC Haplotype Consortium and collaborators.
Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6/MHC.
Location/Qualifiers
1. .156272
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-118E17"
/clone_lib="CHORI-501"
BASE COUNT
41135 a 37989 c 36907 g 40241 t
ORIGIN

Query Match 47.8%; Score 109.4; DB 9; Length 156272;
Best Local Similarity 95.0%; Pred. No. 1.8e-23;
Matches 113; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 60
|||||
Db 25902 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 25843
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QY 61 GCCCCTTGCTCCTCTTGACCCCTCTTGCCAGCTCACAATGGAACAGGCGCGGTATGA 119
|||||
Db 25842 GCCCCTTGCTCCTCTTGACCCCTCTTGCCAGCTCACAATGGAACAGGCTGAGGCTAGA 25784
|||||

RESULT 10
AL713893

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LOCUS       AL713893               178688 bp    DNA    linear    HTG 28-MAR-2002
DEFINITION  Homo sapiens chromosome 6 clone XXbac-307M4, *** SEQUENCING IN
PROGRESS ***, 6 unordered pieces.
ACCESSION   AL713893
VERSION     AL713893.5  GI:19847952
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Sims,S.
TITLE       Direct Submission
JOURNAL     Submitted (26-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
            On Mar 29, 2002 this sequence version replaced gi:19772907.
COMMENT     ----- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            ----- Project Information
            Center project name: bpG307M4
            ----- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 177277 bases at least Q40
            Consensus quality: 177708 bases at least Q30
            Consensus quality: 177956 bases at least Q20
            Insert size: 178180; sum-of-contigs
            Insert size: 192613; 0.9% error; agarose-fp
            Quality coverage: 8.57x in Q20 bases; sum-of-contigs Quality
            coverage: 8.00x in Q20 bases; agarose-fp
            -----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            * 1 37410: contig of 37410 bp in length
            * 37411 37510: gap of 100 bp
            * 37511 82372: contig of 44862 bp in length
            * 82373 82472: gap of 100 bp
            * 82473 142457: contig of 59985 bp in length
            * 142458 142557: gap of 100 bp
            * 142558 152859: contig of 10302 bp in length
            * 152860 152959: gap of 100 bp
            * 152960 172054: contig of 19095 bp in length
            * 172055 172154: gap of 100 bp
            * 172155 178688: contig of 6534 bp in length.

FEATURES             Location/Qualifiers
     source           1..178688
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /clone="XXbac-307M4"
                     /clone.lib="CHORI-501"
     misc_feature     1..37410
                     /note="assembly fragment:03218
                     fragment_chain:1"
     misc_feature     37511..82372
                     /note="assembly fragment:00918
                     fragment_chain:1"
     misc_feature     82473..142457
                     /note="assembly fragment:03231
                     fragment_chain:1"
     misc_feature     142558..152859
                     /note="assembly fragment:03008
                     fragment_chain:1"

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misc_feature       152960..172054
                  /note="assembly fragment:04309
                  fragment_chain:1"
misc_feature       172155..178688
                  /note="assembly fragment:03507
                  fragment_chain:1
                  clone_end:T7
                  vector_side:right"
BASE COUNT        46316 a 40707 c 42166 g 48998 t      501 others
ORIGIN
Query Match       47.8%; Score 109.4; DB 2; Length 178688;
Best Local Similarity 95.0%; Pred. No. 1.8e-23;
Matches 113; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ACCGGACATTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTGGGCT 60
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Db 173451 ACCGGACATTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTGGGCT 173510
      |||||
QY 61 GCCCCTTGCTCCCTCTGACCTCTTGGCAGCTCACATGGACAGCGCGGCTATGA 119
      |||||
Db 173511 GCCCCTTGCTCCCTCTGACCTCTTGGCAGCTCACATGGACAGCGGCTAGA 173569
      |||||

RESULT 11
LOCUS           AB023048               192650 bp    DNA    linear    PRI 20-NOV-1999
DEFINITION     Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
                clone:53L9, complete sequence.
ACCESSION       AB023048
VERSION         AB023048.1  GI:5672603
KEYWORDS        HTG.
SOURCE          Homo sapiens
                Homo sapiens cell_line:978SK DNA, clone:53L9.
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (sites)
AUTHORS         Shihina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
                Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,I.,
                Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
                Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
                Bahram,S. and Inoko,H.
                Molecular dynamics of MHC genesis unraveled by sequence analysis of
                the 1,796,938-bp HLA class I region
                Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
REFERENCE       2 (bases 1 to 192650)
AUTHORS         Shihina,T. and Takishima,N.
TITLE           Direct Submission
JOURNAL         Submitted (29-JAN-1999) Takashi Shihina, Tokai University School of
                Medicine, Department of Molecular Life Science 2; Bohseidai,
                Isehara, Kanagawa 259-1193, Japan
                (E-mail: tshihina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,
                Fax:81-463-94-8884)

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                     /chromosome="6"
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Matches 113; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Query Match 47.8% Score 109.4; DB 9; Length 200000;
Best Local Similarity 95.0%; Pred. No. 1.8e-23;
Matches 113; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 61 GCCCCTTGCTTCCTTGGACCTCTTGGCAGTCCACATGGAACAGCGCGGTATGA 119
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ACCESSION AX344553
VERSION AX344553.1 GI:18492439
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 4 03-JAN-2002;
EpiGenomics AG (DE)
FEATURES
Location/Qualifiers
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/db_xref="taxon:32630"
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BASE COUNT 86882 a 5859 c 85073 g 172166 t
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Matches 81; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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DEFINITION Sequence 5 from Patent WO0200932.
ACCESSION AX344554
VERSION AX344554.1 GI:18492440
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 5 03-JAN-2002;
EpiGenomics AG (DE)
FEATURES
Location/Qualifiers
source 1..349980
/organism="synthetic construct"
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/notes="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows.-seq 01 0.000.001 To 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-Original length of seq 2: 3.673778 <223>-split as follows.-seq 14 0.000.001 To 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 2.749.980-seq 23 2.700.001 3.049.980-seq 24 3.000.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.673.778"

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Query Match      28.8%; Score 66; DB 6; Length 349980;
Best Local Similarity 76.4%; Pred. No. 1e-09;
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ACCESSION	AX344571				
VERSION	AX344571.1	GI:18492457			
KEYWORDS					
SOURCE	synthetic construct.				
ORGANISM	artificial sequences.				
REFERENCE	1.				
AUTHORS	Olek,A., Piepenbrock,C. and Berlin,K.				
TITLE	Diagnosis of known genetic parameters within the mhc				
JOURNAL	Patent: WO 0200932-A 22 03-JAN-2002;				
FEATURES	Epigenomics AG (DE)				
source	Location/Qualifiers				
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	/notes="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 follows.-seq 01 0.000.001 To 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <22>-Original length of seq 2: 3.673778 <22>-split as follows.-seq 14 0.000.001 To 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 2.749.980-seq 23 2.700.001 3.049.980-seq 24 3.000.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.673.778"				
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Job time : 1313.79 secs

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Search completed: May 1, 2003, 04:15:02
Job time : 1313.79 secs

Query Match

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 04:34:36 ; Search time 64.2211 Seconds
(without alignments)
4397.425 Million cell updates/sec

Title: US-09-092-296-1
Perfect score: 239
Sequence: 1 GCCCACGGGACTTCAGTGT.....CCCTTCAGGACGACGCTGA 239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 746064 seqs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	227	95.0	422	9	US-09-992-598-362
4	227	95.0	422	9	US-09-989-293A-362
5	227	95.0	422	9	US-10-063-547-65
6	227	95.0	422	9	US-09-989-735-362
7	227	95.0	422	9	US-09-990-444-362
8	227	95.0	422	9	US-09-989-730-362
9	227	95.0	422	9	US-09-990-436-362
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11	227	95.0	422	9	US-09-993-687-362
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29 227 95.0 422 9 US-09-990-562-362 Sequence 362, App
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31 227 95.0 422 9 US-09-997-666-362 Sequence 362, App
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ALIGNMENTS

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; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:

1: INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
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NAME/KEY: base_polymorphism
LOCATION: 200
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OTHER INFORMATION: T or C polymorphism at this position"

US-09-092-296-1

Query Match 99.6%; Score 238; DB 9; Length 239;
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RESULT 2

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Patent No. US20020188114A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,296
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,810
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6104, US. 01
TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-092-296-2

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Best Local Similarity 99.6%; Pred. No. 2e-67;
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RESULT 3

US-09-992-598-362
Sequence 362, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
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; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478

[illegible]

QY 1 GGCACGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTGTG 60
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Db 8 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTGTG 67
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QY 61 GCGTGGCCCTTGTCTCTTGGACCTCTTGGCAGCTCACATGGACAGGCGCGGTA 120
|||||
Db 68 GCGTGGCCCTTGTCTCTTGGACCTCTTGGCAGCTCACATGGACAGGCGCGGTA 127
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QY 121 TGACTTTGCAACTGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
|||||
Db 128 TGACTTTGCAACTGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 187
|||||
QY 181 TCCTGGAATGCTTGA AAA-NYTCGCTCTCTCTCCATCTCCCTTCAAGGACACGGTCA 239
|||||
Db 188 TCCTGGAATGCTTGA AAAAGCTGTGCTCTCTCTCCATCTCCCTTCAAGGACACGGTCA 247
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RESULT 6
US-09-989-735-362
; Sequence 362, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18

[illegible]

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; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 95.08; Score 227; DB 9; Length 422;
Best Local Similarity 99.28; Pred. No. 5.3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCCCACCAGGACTTCAGTGTCTCTCCATCCAGGAGCCAGTGGCCACTATGGGGTCTG 60
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Db 8 GCCCACCAGGACTTCAGTGTCTCTCCATCCAGGAGCCAGTGGCCACTATGGGGTCTG 67
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QY 61 GCCTGCCCTTGTCTCTCTTGTGACCTCTTGGCAGCTCACATGGAACAGGCCGGGTA 120
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Db 68 GCCTGCCCTTGTCTCTCTTGTGACCTCTTGGCAGCTCACATGGAACAGGCCGGGTA 127
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QY 121 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
|||||

Db 128 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 187
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QY 181 TCCCTGGAATTGCTTGAATAA-NITCTGCCTCTCTCTCCATCTCCCTTCAGGACACCGGTCA 239
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Db 188 TCCCTGGAATTGCTTGAANAAGCTCTGCCTCTCTCCATCTCCCTTCAGGACACCGGTCA 247
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RESULT 9
US-09-990-436-362
; Sequence 362, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC14
; CURRENT APPLICATION NUMBER: US/09/990,436
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/052250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311

[illegible]

RESULT 10

[illegible]

[illegible]

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; PRIOR APPLICATION NUMBER: 60/088858
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; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 95.0%; Score 227; DB 9; Length 422;
Best Local Similarity 99.2%; Pred. No. 5, 3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCCACCGGACTTCAGTGTCTCTCCATCCGAGGAGCGAGTGGCCACTATGGGGTGTG 60
Db 8 GCCACCGGACTTCAGTGTCTCTCCATCCGAGGAGCGAGTGGCCACTATGGGGTGTG 67
QY 61 GCCTGCCCTTGTCTCTCTTGTGACCTCTTGGCAGCTCACATGGAAACAGGCGGGTA 120
Db 68 GCCTGCCCTTGTCTCTCTTGTGACCTCTTGGCAGCTCACATGGAAACAGGCGGGTA 127
QY 121 TCACCTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
Db 128 TCACCTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 187
QY 181 TCCTGGAAATTCCTTGA AAAA -NTCTGCCCTCTCTCTCCATCTCCCTTCAGGGACCGGTCA 239
Db 188 TCCTGGAAATTCCTTGA AAAAGCTCTGCTCTCTCTCTCCATCTCCCTTCAGGGACCGGTCA 247

RESULT 13
US-09-997-653-362
; Sequence 362, Application US/09997653
; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match          95.0%; Score 227; DB 9; Length 422;
Best Local Similarity 99.2%; Pred. No. 5.3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY 1 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 60
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Db 8 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 67

QY 61 GGCTGCCCTTCTCTCTCTTGACCTCTTGCGAGCTCACATGGAACAGGCGGGTA 120
   |||||||
Db 68 GGCTGCCCTTCTCTCTCTTGACCTCTTGCGAGCTCACATGGAACAGGCGGGTA 127

QY 121 TGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
   |||||||
Db 128 TGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 187

QY 181 TCCTGGAATGTTGAAA-NCTGCTCCTCTCCATCTCCCTTCAGGACCGCGTCA 239
   |||||||
Db 188 TCCTGGAATGTTGAAAAGCTGCTCCTCTCCATCTCCCTTCAGGACCGCGTCA 247
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RESULT 14

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US-10-174-590-241
; Sequence 241, Application US/10174590
; Publication No. US2003008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-241
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Query Match          95.0%; Score 227; DB 9; Length 422;
Best Local Similarity 99.2%; Pred. No. 5.3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY 1 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 60
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QY 61 GGCTGCCCTTCTCTCTCTTGACCTCTTGCGAGCTCACATGGAACAGGCGGGTA 120
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QY 121 TGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
   |||||||
Db 128 TGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 187

QY 181 TCCTGGAATGTTGAAA-NCTGCTCCTCTCCATCTCCCTTCAGGACCGCGTCA 239
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Db 188 TCCTGGAATGTTGAAAAGCTGCTCCTCTCCATCTCCCTTCAGGACCGCGTCA 247
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RESULT 15

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US-10-176-758-241
; Sequence 241, Application US/10176758
; Publication No. US2003008353A1
; GENERAL INFORMATION:
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior application removed - See File Wrapper or Palm
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; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-758-241
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Query Match          95.0%; Score 227; DB 9; Length 422;
Best Local Similarity 99.2%; Pred. No. 5.3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY 1 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 60
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Db 8 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 67

QY 61 GGCTGCCCTTGTCTCTCTTGACCTCTTGCGAGCTCACATGGAACAGGCGGGTA 120
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Db 68 GCGTGCCCTTGTCCTCTTGACCCCTTGGCAGCTCACATGGAACAGGGCGGGTA 127
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Db 128 TGACTTTGCACTGAGCTGAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 187
QY 181 TCCTGGAAATGGCTTGA AAA - NTCTGCCCTCCTCCATCTCCCTTCAGGACCCAGCGTCA 239
Db 188 TCCTGGAAATGGCTTGA AAAAGCTGTGCCCTCCTCCATCTCCCTTCAGGACCCAGCGTCA 247
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Search completed: May 1, 2003, 05:17:08
Job time : 68.2211 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 03:53:25 ; Search time 43.356 Seconds
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Title: US-09-092-296-1

Perfect score: 239

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Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	30.4	12.7	580	3	US-08-817-436A-1
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16	29	12.1	1316	4	US-09-056-105-24
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19	29	12.1	2259	6	US-08-910-990-8
20	29	12.1	2564	3	US-08-276-968A-19
21	28.8	12.1	1785	3	US-08-729-416C-8
22	28.2	11.8	3218	4	US-09-369-364A-6
23	27.8	11.6	1396	4	US-09-328-174A-2
24	27.8	11.6	2870	4	US-09-221-017B-850
25	27.8	11.6	8396	4	US-09-328-174A-1
26	27.8	11.6	8409	4	US-09-167-681-37
27	27.6	11.5	956	4	US-09-641-638-36

c 28	27.6	11.5	956	4	US-09-641-638-37	Sequence 37, Appl
c 29	27.6	11.5	956	4	US-09-641-638-38	Sequence 36, Appl
c 30	27.6	11.5	956	4	US-09-641-638-39	Sequence 39, Appl
c 31	27.6	11.5	1001	4	US-09-641-638-628	Sequence 628, Appl
c 32	27.6	11.5	1294	2	US-08-665-647-4	Sequence 4, Appl
c 33	27.6	11.5	3088	1	US-08-418-444-1	Sequence 1, Appl
c 34	27.6	11.5	5102	1	US-08-494-168-1	Sequence 1, Appl
c 35	27.6	11.4	956	4	US-09-641-638-40	Sequence 40, Appl
c 36	27.2	11.4	1295	4	US-09-219-194-3	Sequence 3, Appl
c 37	27.2	11.4	2122	1	US-08-485-449-1	Sequence 12, Appl
c 38	27.2	11.4	3398	5	PCT-US95-08493-12	Sequence 1, Appl
c 39	27.2	11.4	20674	4	US-09-641-638-651	Sequence 651, App
c 40	27.2	11.4	152331	3	US-09-128-155-16	Sequence 16, Appl
c 41	27.2	11.4	176373	3	US-09-128-155-17	Sequence 17, Appl
c 42	27	11.3	1593	2	US-08-878-989-9	Sequence 9, Appl
c 43	27	11.3	1593	4	US-09-272-796-9	Sequence 9, Appl
c 44	27	11.3	1833	4	US-09-344-700-3	Sequence 3, Appl
c 45	27	11.3	9721	4	US-09-345-217-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-817-436A-1
; Sequence 1, Application US/08817436A
; Patent No. 5882880
; GENERAL INFORMATION:
; APPLICANT: Canaan, Dan
; TITLE OF INVENTION: Human Checkpoint Gene and Gene for
; TITLE OF INVENTION: Antisense RNA thereof
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wiman, Cohen, Leitner & Myers
; STREET: 900 17th Street, N.W., Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch, 1.44Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,436A
FILING DATE: 11-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12445
FILING DATE: 11-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Herbert
REGISTRATION NUMBER: 25,109
REFERENCE/DOCKET NUMBER: 0744.066
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-463-7700
TELEFAX: 202-463-6915
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3509 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: ESTABLISHED XERODERMA PIGMENTOSUM GM2096-SV3
IMMEDIATE SOURCE:
CLONE: RAP-1 cDNA

US-08-817-436A-1

APPLICATION NUMBER: US/08/822,936
FILING DATE: 21-FEBRUARY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-079.05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 580 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 91..480
US-08-822-936-7

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Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 39 GCAGTGGCCACTATGGGTCTGGGCTGCCCTTGTCTCTCTTGAACCTCTCTTGGCAGC 98
Db 128 GCGGTGGCCAGGCCCGCGCTCACTGCTGCCGCCAACATGCGCTTGTCCCGGGTCTGTGGC 69
QY 99 TCACATGGAACAGGCCGCGGTATGACTTTTGAACATG 134
Db 68 AGAAATGGTCTTCGCCGCCGTGAGATTGCTACAG 33

RESULT 7
US-08-497-214D-7/c
; Sequence 7, Application US/08497214D
; Patent No. 6331390
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,214D
; FILING DATE: 30-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both

; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..480
; US-08-497-214D-7

Query Match 12.7%; Score 30.4; DB 4; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.8;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 39 GCAGTGGCCACTATGGGTCTGGGCTGCCCTTGTCTCTCTTGAACCTCTCTTGGCAGC 98
Db 128 GCGGTGGCCAGGCCCGCGCTCACTGCTGCCGCCAACATGCGCTTGTCCCGGGTCTGTGGC 69
QY 99 TCACATGGAACAGGCCGCGGTATGACTTTTGAACATG 134
Db 68 AGAAATGGTCTTCGCCGCCGTGAGATTGCTACAG 33

RESULT 8
PCT-US95-04636-7/c
; Sequence 7, Application PC/TUS9504636
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04636
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both


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; Patent No. 6329171
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 23484, A NOVEL HUMAN UBIQUITIN
; FILE REFERENCE: 5800-51
; CURRENT APPLICATION NUMBER: US/09/408,865A
; CURRENT FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3941
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (279)...(3650)
; US-09-408-865-2

Query Match      12.2%; Score 29.2; DB 4; Length 3941;
Best Local Similarity 57.8%; Pred. NO. 4.7;
Matches 52; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGCTG 60
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Db 2892 GGTCCAGCGGTGTCTGTGTCTGTGCCCCCTCTGCGGGCGCTGGCAGCTGTGCTCCG 2833

QY 61 GCGTGGCCCTTGCTCTCTCTTGACCTCC 90
    ||| ||| ||| ||| ||| ||| ||| |||
Db 2832 GCGCGCTTCTTCTTCTCTCTCTCTCTCC 2803

RESULT 15
US-07-709-949-1
; Sequence 1, Application US/07709949
; Patent No. 5472858
; GENERAL INFORMATION:
; APPLICANT: Attie, Alan D
; APPLICANT: Gretsch, Daniel G
; APPLICANT: Sturley, Stephen L
; APPLICANT: Beckage, Nancy E
; TITLE OF INVENTION: Production of Recombinant Proteins in
; TITLE OF INVENTION: Insect Larvae
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: P.O. Box 2113
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/709,949
; FILING DATE: 19910604
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 9629691801
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1157 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 62...1015
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 62...119
; PUBLICATION INFORMATION:
; AUTHORS: McLean, J W
; JOURNAL: Journal of Biological Chemistry
; VOLUME: 259
; PAGES: 6498-6504
; DATE: 1984
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1157
; US-07-709-949-1

Query Match      12.1%; Score 29; DB 1; Length 1157;
Best Local Similarity 54.1%; Pred. NO. 3.2;
Matches 59; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 10 GACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGTCTGGGCTGCCCC 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 626 GAGCGGGGCTCAGCGCCATCCGAGAGCCCTGGGGCCCTGGTGGAAACAGGCGCGGTG 685

QY 70 TTGTCTCTCTTTGACCTCTCTTGGCAGCTCATATGGAACAGGCGCGGG 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 686 CGGGCGGCCACTGTGGGTCTCTCTGGCCGCCAGCGCTACAGGAGCGGG 734

Search completed: May 1, 2003, 05:13:03
Job time : 58.356 secs

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GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 03:08:45 ; Search time 1196.9 Seconds
(without alignments)
3233.964 Million cell updates/sec

Title: US-09-092-296-1
Perfect score: 239
Sequence: 1 GGCCACGGACTTCAGTGT.....CCCTTCAGGACCGCGTCA 239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	225.4	94.3	449	10 AW293443	AW293443 UI-H-B12-
2	225.4	94.3	830	13 BI759796	BI759796 603045679
3	220	92.1	455	12 BG506690	BG506690 601861290
c 4	219	91.6	422	12 BF002050	BF002050 7998c11.x
5	137.6	57.6	865	13 BI820110	BI820110 603037110
6	137.2	57.4	895	13 BI820029	BI820029 603037210

c 7	118	49.4	404	9 AI857998	AI857998 wj69b01.x
8	95.8	40.1	521	10 BB533837	BB533837 BB533837
9	95.8	40.1	522	10 BB664284	BB664284 BB664284
10	94	39.3	361	12 BF521842	BF521842 UI-R-C2p-
c 11	74.4	31.1	552	17 AQ718761	AQ718761 HS_5511_B
c 12	63.6	26.6	328	9 AI136523	AI136523 UI-R-C2p-
c 13	44.6	18.7	506	17 AZ241329	AZ241329 RPCI-23-7
c 14	44.6	18.7	633	17 AZ079350	AZ079350 RPCI-23-4
c 15	36	15.1	754	12 BG686317	BG686317 602638230
16	35.6	14.9	1020	13 BM477469	BM477469 AGENCOURT
17	35.6	14.9	509	17 AO838514	AO838514 HS_5011_A
18	35.6	14.9	1019	13 BM474221	BM474221 AGENCOURT
19	35	14.6	348	14 F06958	F06958 HSC10C101.n
c 20	34.6	14.5	261	10 BB411111	BB411111 BB411111
21	34.4	14.4	238	9 AA376266	AA376266 EST88915
c 22	34.4	14.4	264	14 BQ377407	BQ377407 IL5-UM007
c 23	34.4	14.4	412	9 AA769782	AA769782 ah71b05.s
c 24	34.4	14.4	458	9 AI632159	AI632159 ts85e12.x
c 25	34.4	14.4	470	9 AI803529	AI803529 tc42h11.x
c 26	34.4	14.4	516	10 BE613876	BE613876 601504121
c 27	34.4	14.4	543	10 AW851149	AW851149 IL3-C7022
28	34.4	14.4	753	13 BI911665	BI911665 603064838
29	34.4	14.4	783	10 BE563718	BE563718 601333355
30	34.4	14.4	785	13 BI193645	BI193645 602946554
31	34.4	14.4	788	12 BG762871	BG762871 602735108
32	34.4	14.4	828	12 BG768039	BG768039 602743815
33	34.4	14.4	837	13 BM449774	BM449774 AGENCOURT
34	34.4	14.4	871	14 BQ956320	BQ956320 AGENCOURT
35	34.4	14.4	931	12 BF689789	BF689789 602186518
36	34.4	14.4	954	14 BQ220846	BQ220846 AGENCOURT
37	34.4	14.4	959	14 BQ940113	BQ940113 AGENCOURT
38	34.4	14.4	999	9 AL551231	AL551231 AL551231
39	34.4	14.4	1013	14 BQ953477	BQ953477 AGENCOURT
40	34.4	14.4	1061	14 BQ052186	BQ052186 AGENCOURT
41	34.4	14.4	1129	13 BM464458	BM464458 AGENCOURT
42	34.4	14.4	1138	13 BM564409	BM564409 AGENCOURT
43	34.4	14.4	1232	14 BM911289	BM911289 AGENCOURT
c 44	34	14.2	271	17 BH244391	BH244391 NTZEB57TF
45	34	14.2	575	13 BI223412	BI223412 602943001

ALIGNMENTS

RESULT 1
AW293443/c
LOCUS AW293443 449 bp mRNA linear EST 16-JAN-2000
DEFINITION UI-H-B12-ahm-c-08-0-UI.sl NCI_CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2727182 3', mRNA sequence.
ACCESSION AW293443
VERSION AW293443.1 GI:6700079
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 449)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/hcicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library Preparation: M.B. Soares Lab Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=yes.

Location/Qualifiers

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source
1. .449
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2727182"
/lab_host="NCI_CGAP_Sub4"
/notes="Vector: pF73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI_CGAP_Sub4 library is a subtracted library derived from
the NCI_CGAP_Sub2 library which is a subtracted library
derived from the NCI_CGAP_Sub1 library, which is a
subtracted library derived from BI. BI constitutes a
mixture of 21 normalized or subtracted NCI_CGAP
libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28,
NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5,
NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11,
NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1,
NCI_CGAP_Le12, NCI_CGAP_Brn23, NCI_CGAP_Lu5,
NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 : LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE Clonoids 1322376-1323911,
1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 :
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids
1323912-1325831, 1471368-1472903, 1492104-1493255)
NCI_CGAP_Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE
Clonoids 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4
pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
Clonoids 1257096-1258631, 1469064-1470983, 1475592-1476743
) NCI_CGAP_Pr22 pool 1 : LLAM 2457-2459, 2758-2759,
3062-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959,
1219728-1220615) NCI_CGAP_Co10 pool 1 : LLAM 2644-2653,
2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145351
) Subtraction was performed as previously described
[Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
Genome Research 6, 791-806.]
TAG_LIB=NCI_CGAP_Co4
TAG_ISSUE=colon
TAG_SEQ=CTTCG"
BASE COUNT 104 a 108 c 134 g 103 t
Query Match 94.3%; Score 225.4; DB 10; Length 449;
Best Local Similarity 98.8%; Pred No. 4.3e-54;
Matches 237; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 60
|||||
Db 437 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 378
|||||
QY 61 GGCTGCCCTTGTCTCTCTTACCTCTTGGCAGCTCACATGGAACAGGCGCGGTA 120
|||||
Db 377 GGCTGCCCTTGTCTCTCTTACCTCTTGGCAGCTCACATGGAACAGGCGCGGTA 318
|||||
QY 121 TGACTTTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCT 180
|||||
Db 317 TGACTTTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCT 258
|||||
QY 181 TCCTGGAATTCCTGAAAA-NCTCGCTCCCTCCATCTCCCTTCAGGACCGCGTCA 239
|||||
Db 237 TCCTGGAATTCCTGAAAACTCTGCTCTCTCTCCATCTCCCTTCAGGACCGCGTCA 198
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RESULT 2
BI759796 830 bp mRNA linear EST 25-SEP-2001
LOCUS 603045679F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186107 5',
DEFINITION mRNA sequence.
ACCESSION BI759796
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VERSION BI759796.1 GI:15751374
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL 1 (bases 1 to 830)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11464 Row: m column: 20
High quality sequence stop: 432.
Location/Qualifiers
1. .830
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/db_xref="taxon:9606"
/clone="IMAGE:5186107"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/notes="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 175 a 276 c 210 g 168 t 1 others
ORIGIN
Query Match 94.3%; Score 225.4; DB 13; Length 830;
Best Local Similarity 98.8%; Pred No. 5.5e-54;
Matches 237; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 60
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Db 31 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 90
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QY 61 GGCTGCCCTTGTCTCTCTTACCTCTTGGCAGCTCACATGGAACAGGCGCGGTA 120
|||||
Db 91 GGCTGCCCTTGTCTCTCTTACCTCTTGGCAGCTCACATGGAACAGGCGCGGTA 150
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QY 121 TGACTTTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCT 180
|||||
Db 151 TGACTTTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCT 210
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QY 181 TCCTGGAATTCCTGAAAA-NCTCGCTCCCTCCATCTCCCTTCAGGACCGCGTCA 239
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Db 211 TCCTGGAATTCCTGAAAAAGCTCTGCTCTCTCTCCATCTCCCTTCAGGACCGCGTCA 270
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RESULT 3
BI506690 456 bp mRNA linear EST 27-MAR-2001
LOCUS 601861290F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4070759 5',
DEFINITION mRNA sequence.
ACCESSION BI506690
VERSION BI506690
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Clontech Laboratories, Inc.
CDNA Library Preparation: Clontech Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLC915 row: d column: 24
High quality sequence stop: 401.
Location/Qualifiers
1..456
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4070759"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pBMR-LIB (Clontech); Site: 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
BASE COUNT 109 a 137 c 106 g 103 t 1 others
ORIGIN
Query Match 92.1%; Score 220; DB 12; Length 456;
Best Local Similarity 99.1%; Pred. No. 1.5e-52;
Matches 231; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 8 GGGACTTCAGTCTCTCCATCCAGAGCGCAGTGGCCACTATGGGTCTGGGCTGCC 67
Db 2 GGGACTTCAGTCTCTCCATCCAGAGCGCAGTGGCCACTATGGGTCTGGGCTGCC 61
QY 68 CTTGTCTCTTTCAGCTCTCTTGGCAGCTCAGATGGACAGGCGCGGTATGACTTT 127
Db 62 CTTGTCTCTTTCAGCTCTCTTGGCAGCTCAGATGGACAGGCGCGGTATGACTTT 121
QY 128 GCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCTGGA 187
Db 122 GCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCTGGA 181
QY 188 ATTGCTTGAAGA--NCTGCTCTCTCTCCATCTCCCTTCAGGACACAGGTCA 239
Db 182 ATTGCTTGAAGAAGCTCTGCTCTCTCTCCATCTCCCTTCAGGACACAGGTCA 234
RESULT 4
BF002050/c 422 bp mRNA linear EST 06-OCT-2000
LOCUS 7998c11.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:3314516 3',
DEFINITION mRNA sequence.
ACCESSION BF002050
VERSION BF002050.1 GI:10702325
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 422)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..422
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3314516"
/clone_lib="NCI_CGAP_Col6"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pF7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Col40 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 102 a 99 c 130 g 88 t 3 others
ORIGIN
Query Match 91.6%; Score 219; DB 12; Length 422;
Best Local Similarity 98.3%; Pred. No. 2.9e-52;
Matches 232; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
QY 6 CCGGGACTTCAGTCTCTCCATCCAGAGCGCAGTGGCCACTATGGGTCTGGGCTG 65
Db 422 CCGGGANTTTCAGTCTCTCTCCATCCAGAGCGCAGTGGCCACTATGGGTCTGGGCTG 363
QY 66 CCCCTGTCTCTCTCTTGACCCCTCTTGACAGCTCACATGGAACAGGCGCGGTATGACT 125
Db 362 CCCCTGTCTCTCTCTTGACCCCTCTTGACAGCTCACATGGAACAGGCGCGGTATGACT 303
QY 126 TTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCTG 185
Db 302 TTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCTG 243
QY 186 GAATTGCTTGAAGA--NCTGCTCTCTCTCCATCTCCCTTCAGGACACAGGTCA 239
Db 242 GAATTGCTTGAAGAAGNTGCTCTCTCTCCATCTCCCTTCAGGACACAGGTCA 187
RESULT 5
BI820110 865 bp mRNA linear EST 04-OCT-2001
LOCUS 603037110F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178170 5',
DEFINITION mRNA sequence.
ACCESSION BI820110
VERSION BI820110.1 GI:15931660
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 865)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

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/clone_lib="NCI_CGAP_Lu19"
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LOCUS	BB564284	522 bp	mRNA	linear	EST 26-OCT-2001
DEFINITION	BB564284 RIKEN full-length enriched, 0 day neonate lung Mus musculus cDNA clone E030032D13 5', mRNA sequence.				
ACCESSION	BB564284				
VERSION	BB564284.1	GI:16498038			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 522)				
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanazaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ono,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.				
TITLE	RIKEN Mouse ESTs (Arakawa,T. et al. 2001)				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues. Location/Qualifiers 1. 522 /organism="Mus musculus" /db_xref="taxon:10090" /clone="E030032D13" /clone_lib="RIKEN full-length enriched, 0 day neonate lung" /tissue_type="lung" /dev_stage="0 day neonate" /db_host="Dhl08" /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCACTGCGATTTTTTTTTTNN 3'] cDNA was prepared by using trihalose thermo-activated reverse				

Plate: 438 row: H column: 19

Seq primer: T7

Class: BAC ends

Location/Qualifiers
1..633

/organism="Mus musculus"
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/clone="RPCI-23-438H19"
/clone_lib="RPCI-23"
/sex="Female"
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/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 138 a 191 c 161 g 143 t
ORIGIN

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Best Local Similarity 68.1%; Pred. NO. 0.029;
Matches 62; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 109 CAGGCGGGTATGACTTGCACCTGAAGCTCAGGAGTCTTTCTGACAAATTCCTCCT 168

Db 403 CAGGCGAAGGTGATTCGAGTAAGCTGACCGAGACTTTTCAGGACAGACCTCCC 344

QY 169 ATGAGTCCAGCTTCTCGAATTCGTTCAAAA 199

Db 343 AGAACTCCAGTCTCTGGACATGCTCAAAA 313

RESULT 15
BG686317
LOCUS 754 bp mRNA linear EST 01-MAY-2001
DEFINITION 602638230F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765975 5',
mRNA sequence.

ACCESSION BG686317

VERSION BG686317.1 GI:13917714

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 754)
NIH-MGC <http://mhc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM1625 row: 1 column: 08
High quality sequence stop: 750.
Location/Qualifiers
1..754

FEATURES
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/organism="Homo sapiens"
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/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 166 a 206 c 201 g 181 t
ORIGIN

Query Match 15.1%; Score 36; DB 12; Length 754;
Best Local Similarity 64.3%; Pred. No. 8.9;
Matches 54; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 18 TGTCTCTCCATCCACGAGCGCAGTGGCCACTATGGGGTCTGGGGTGCCTTGTCTCTC 77

Db 249 TGTGTCTCTCCCTCCAGGATCCCTTTGGTGTAGTATGGTTCAGGATGCACCATCAC 308

QY 78 CTCTTGACCCCTCCTTGGCAGCTCA 101

Db 309 CTCTAGATACCTTCAGGCAACACA 332

Search completed: May 1, 2003, 05:10:01
Job time : 1207.4 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:55:40 ; Search time 164.211 Seconds
(without alignments)
3277.661 Million cell updates/sec

Title: US-09-092-296-1
Perfect score: 239
Sequence: 1 GGCACCGGACTTCAGTGT.....CCCTTCAGGACCGCTCA 239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	227	95.0	422	21	AA265087
2	227	95.0	422	22	AA546045
3	227	95.0	422	22	AAF92090
4	227	95.0	422	22	AAF44233
5	227	95.0	431	21	AA298124
6	227	95.0	439	20	AAV84366
7	119	49.8	524	24	ABK81818
8	109.8	45.9	729	23	AA565519
9	34.4	14.4	2923	20	AAK04326

10	34.4	14.4	3417	22	AAK94567	Human full-length
11	34	14.2	27082	21	AAK70447	Human immune/haema
12	33.4	14.0	361	21	AAK30979	Human secreted pro
13	33	13.8	6855	24	ABN83971	Human gene sequenc
14	32	13.4	1128	19	AAV28846	Mouse coxsackievir
15	31.8	13.3	1251	24	ABK09969	Eastern cottonmout
16	31.6	13.2	1243	22	AAH42525	Partial cDNA sequen
17	31.6	13.2	1498	22	AAH42526	Nucleotide sequenc
18	31.6	13.2	11749	22	AAK36066	Human musculoskele
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20	31.6	13.2	11749	22	AAK36066	Human reproductive
21	31.6	13.2	11749	22	AAK36066	Human immune/haema
22	31.6	13.2	30420	22	AAK64782	Human musculoskele
23	31.6	13.2	30420	22	AAK64782	DNA encoding human
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25	31.4	13.1	1206	22	AAH94515	Human foetal cDNA,
26	31.2	13.1	705	22	AAH03213	Human cDNA clone (
27	31.2	13.1	2135	22	AAH13650	Human cDNA sequenc
28	31.2	13.1	2644	23	ABL09867	Drosophila melanog
29	31.2	13.1	6096	23	ABL09866	Human immune/haema
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32	31	13.0	3510	17	AAT18696	Human foetal liver
33	30.6	12.8	138	22	ABA70260	Probe #15444 for g
34	30.6	12.8	138	22	ABA36978	Human brain expres
35	30.6	12.8	138	22	AAK18487	Human bone marrow
36	30.6	12.8	138	22	AAK44398	Probe #14784 for g
37	30.6	12.8	138	22	AAK44398	Probe #19080 used
38	30.6	12.8	138	22	AAI50394	Human genome-deriv
39	30.6	12.8	138	24	ABSI8633	Toxicologically re
40	30.6	12.8	180	24	ABSI8633	Human digestive sy
41	30.6	12.8	332	22	AAK87952	Human digestive sy
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ALIGNMENTS

RESULT 1	
AA265087	AA265087 standard; cDNA; 422 BP.
XX	AA265087;
AC	AA265087;
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DT	05-APR-2000 (first entry)
XX	
DE	Membrane-bound protein PRO1098 encoding cDNA.
XX	
DE	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW	pharmaceutical; receptor immunoadhesin; gene mapping; ss.
KW	
OS	Homo sapiens.
XX	
PN	WO9963088-A2.
XX	
PD	09-DEC-1999.
XX	
PF	02-JUN-1999; 99WO-US12252.
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PR	02-JUN-1998; 98US-0087607.
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PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.

(GETH) GENENTECH INC.

PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;

XX WPI; 2000-072883/06.
XX P-PSDB; AAY66741.

XX Membrane-bound proteins and related nucleotide sequences -

PS Claim 2; Fig 257; 822pp; English.

CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be

CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially
 CC by recombinant techniques.

XX SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 95.0%; Score 227; DB 21; Length 422;
 Best Local Similarity 99.2%; Pred. No. 2e-62;
 Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GGCACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTG 60
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RESULT 2

IDS AAS46045

XX AAS46045 standard; cDNA; 422 BP.

XX AC AAS46045;

XX DT 18-DEC-2001 (first entry)

XX DE Human DNA encoding PRO polypeptide sequence #121.

XX KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;

XX KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; cervix; rectum; liver; genetic disorder;
 KW PCR primer.

XX OS Homo sapiens.

XX PN W020016848-A2.

XX PD 20-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US06520.

XX PR 01-MAR-2000; 2000WO-US05601.

XX PR 02-MAR-2000; 2000WO-US05641.

XX PR 03-MAR-2000; 2000US-187202P.

XX PR 06-MAR-2000; 2000US-186968P.

XX PR 14-MAR-2000; 2000US-189320P.

XX PR 14-MAR-2000; 2000US-189320P.

XX PR 15-MAR-2000; 2000WO-US06884.

XX PR 21-MAR-2000; 2000US-190828P.

XX PR 21-MAR-2000; 2000US-191007P.

XX PR 21-MAR-2000; 2000US-191048P.

XX PR 21-MAR-2000; 2000US-191314P.

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XX PR 04-APR-2000; 2000WO-US08439.

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 PR 25-APR-2000; 2000US-199397P.
 PR 25-APR-2000; 2000US-199550P.
 PR 25-APR-2000; 2000US-199654P.
 PR 03-MAY-2000; 2000US-201516P.
 PR 17-MAY-2000; 2000WO-US13705.
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 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
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 PR 28-JUL-2000; 2000WO-US20710.
 PR 22-AUG-2000; 2000US-0644848.
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 PR 08-NOV-2000; 2000WO-US30952.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;

Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI: 2001-602746/68.

P-PSDB; AAU29144.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -

Claim 2; Fig 241; 774pp; English.

Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.

Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 95.0%; Score 227; DB 22; Length 422;

Best Local Similarity 99.2%; Pred. No. 2e-62;

Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GGCACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTG 60

Db 8 GGCACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTG 67

Qy 61 GGTCTCCCTTGTCTCTCTCTGACCCCTCTTGGCAGCTCACATGGAACAGGCCGGTA 120

Db 68 GGTCTCCCTTGTCTCTCTCTGACCCCTCTTGGCAGCTCACATGGAACAGGCCGGTA 127

Qy 121 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCT 180

Db 128 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCT 187

Qy 181 TCTTGAATTCCTTGAAAA-NTCCTCCCTCTCTCCATCTCCCTTCAGGAGCAGCTCA 239

Db 188 TCTTGAATTCCTTGAAAAAGCTCTCCCTCTCTCCATCTCCCTTCAGGAGCAGCTCA 247

```
RESULT 3
AAF92090
ID AAF92090 standard; cDNA; 422 BP.
XX
AC AAF92090;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1098 cDNA.
XX
KW Human; PRO protein; mapping; ss.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23328.
XX
PR 01-SEP-1999; 99WO-US20111.
XX
PR 15-SEP-1999; 99WO-US21090.
XX
PR 07-DEC-1999; 99US-0169495.
XX
PR 09-DEC-1999; 99US-0170262.
XX
PR 11-JAN-2000; 2000US-0175481.
XX
PR 18-FEB-2000; 2000WO-US04341.
XX
PR 18-FEB-2000; 2000WO-US04342.
XX
PR 22-FEB-2000; 2000WO-US04414.
XX
PR 01-MAR-2000; 2000WO-US05601.
XX
PR 03-MAR-2000; 2000US-0187202.
XX
PR 25-APR-2000; 2000US-0199397.
XX
PR 22-MAY-2000; 2000WO-US14042.
XX
PR 05-JUN-2000; 2000US-0209832.
XX
PA (GETH ) GENENTECH INC.
XX
PI Eaton DL, Flivaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2001-183260/18.
XX
DR P-PSDB; AAB87558.
XX
XX Eighty four nucleic acids encoding PRO polypeptides, useful in
XX molecular biology, including use as hybridization probes, and in
XX chromosome and gene mapping.
XX
XX Claim 2; Fig 65; 278pp; English.
XX
CC The present sequence is the coding sequence for a human PRO polypeptide
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC antagonists or anti-PRO antibodies are useful for preparation of a
CC medicament useful in the treatment of a condition which is responsive to
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping.
XX
XX Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;
XX
XX Query Match 95.0%; Score 227; DB 22; Length 422;
XX Best Local Similarity 99.2%; Pred. No. 2e-62;
XX Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 1 GGCCACCGGACTTCAGTGTCCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCGTG 60
DB 8 GGCCACCGGACTTCAGTGTCCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCGTG 67
OY 61 GGTGCGCCCTTGTCCTCTTGACCCCTTGGCAGCTCACATGGACACAGGCGCGGTA 120
DB 68 GGTGCGCCCTTGTCCTCTTGACCCCTTGGCAGCTCACATGGACACAGGCGCGGTA 127

OY 121 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCT 180
DB 128 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCT 187
OY 181 TCCTGGAATTCCTTGAAAA-NCTGCGCTCCCTCCATCTCCCTTCAGGACACAGCGTCA 239
DB 188 TCCTGGAATTCCTTGAAAAAGCTCTGCTCCTCCTCTCCATCTCCCTTCAGGACACAGCGTCA 247

RESULT 4
AAF44233
ID AAF44233 standard; cDNA; 422 BP.
XX
AC AAF44233;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1098 (UNQ541) nucleotide sequence SEQ ID NO:362.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay; ss.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
XX
PR 23-JUN-1999; 99US-0141037.
XX
PR 07-JUL-1999; 99US-0143048.
XX
PR 20-JUL-1999; 99US-0144758.
XX
PR 26-JUL-1999; 99US-0145698.
XX
PR 28-JUL-1999; 99US-0148222.
XX
PR 17-AUG-1999; 99US-0149396.
XX
PR 15-SEP-1999; 99WO-US21090.
XX
PR 08-OCT-1999; 99US-0158663.
XX
PR 30-NOV-1999; 99WO-US28313.
XX
PR 01-DEC-1999; 99WO-US28301.
XX
PR 16-DEC-1999; 99WO-US30095.
XX
PR 20-DEC-1999; 99WO-US30911.
XX
PR 05-JAN-2000; 2000WO-US00219.
XX
PR 06-JAN-2000; 2000WO-US00376.
XX
PR 11-FEB-2000; 2000WO-US03565.
XX
PR 18-FEB-2000; 2000WO-US04341.
XX
PR 22-FEB-2000; 2000WO-US04414.
XX
PR 24-FEB-2000; 2000WO-US04914.
XX
PR 24-FEB-2000; 2000WO-US05004.
XX
PR 02-MAR-2000; 2000WO-US05841.
XX
PR 15-MAR-2000; 2000WO-US06884.
XX
PR 20-MAR-2000; 2000WO-US07377.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Kljavin LJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX
XX WPI; 2001-032160/04.
XX P-PSDB; AAB65264.
XX
XX PRO polynucleotides used to produce polypeptides used to target
XX bioactive molecules such as toxins, radiolabels or antibodies, to
XX specific cells, to cause targeted cell death -
XX
XX Claim 2; Fig 257; 935pp; English.
```

XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 95.0%; Score 227; DB 22; Length 422;
Best Local Similarity 99.2%; Pred. No. 2e-62;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GGCCACGGGAGTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCG 60
|||||
DB 8 GGCCACGGGAGTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCG 67
|||||
QY 61 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGGCAGCTCACATGGAAACAGGCGCGGTA 120
|||||
DB 68 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGGCAGCTCACATGGAAACAGGCGCGGTA 127
|||||
QY 121 TGACTTGGCACTGAAGCTGAAGGAGTCTTTCTGACAAATCTCTATGAGTCCAGCT 180
|||||
DB 128 TGACTTGGCACTGAAGCTGAAGGAGTCTTTCTGACAAATCTCTATGAGTCCAGCT 187
|||||
QY 181 TCCTGGAATGCTTGA AAAA-NTCTGCCTCTCTCTCCATCCAGGAGCGCAGGTCA 239
|||||
DB 188 TCCTGGAATGCTTGA AAAAGCTCTGCTCTCTCTCCATCCAGGAGCGCGTCA 247
|||||

RESULT 5
AAZ98124
ID AAZ98124 standard; cDNA; 431 BP.
XX
AC AAZ98124;
XX
XX 11-MAY-2000 (first entry)
DE Human signal peptide containing protein HSP-16 cDNA SEQ ID NO:150.
XX
KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's disease; ovulatory defect;
muscular dystrophy; ss.
XX
OS Homo sapiens.
XX
PN WO200000610-A2.
XX
PD 06-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14484.
XX
PR 26-JUN-1998; 98US-0090762.
XX 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX
XX (INCY-) INCYTE PHARM INC.

XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX WPI: 2000-160673/14.
DR P-PSDB; AAY87239.
XX
XX New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
PS Claim 9; Page 261; 327pp; English.
XX
XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. HSPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, or
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. HSP are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSP
CC from natural sources.
XX
SQ Sequence 431 BP; 93 A; 135 C; 101 G; 102 T; 0 other;

Query Match 95.0%; Score 227; DB 21; Length 431;
Best Local Similarity 99.2%; Pred. No. 2.1e-62;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GGCCACGGGAGTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCG 60
|||||
DB 1 GGCCACGGGAGTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCG 60
|||||
QY 61 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGGCAGCTCACATGGAAACAGGCGCGGTA 120
|||||
DB 61 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGGCAGCTCACATGGAAACAGGCGCGGTA 120
|||||
QY 121 TGACTTGGCACTGAAGCTGAAGGAGTCTTTCTGACAAATCTCTATGAGTCCAGCT 180
|||||
DB 121 TGACTTGGCACTGAAGCTGAAGGAGTCTTTCTGACAAATCTCTATGAGTCCAGCT 180
|||||
QY 181 TCCTGGAATGCTTGA AAAA-NTCTGCCTCTCTCTCCATCCAGGAGCGCGTCA 239
|||||
DB 181 TCCTGGAATGCTTGA AAAAGCTCTGCTCTCTCTCCATCCAGGAGCGCGTCA 240
|||||

RESULT 6
AAV84366
ID AAV84366 standard; cDNA to mRNA; 439 BP.
XX
AC AAV84366;
XX
XX 30-MAR-1999 (first entry)
DT Human stomach carcinoma cDNA clone HP10408.
XX
DE Transmembrane protein; HP10408; human; stomach cancer; ds.
KW

the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in (see AAX04311 for described uses).

PR	05-SEP-2000;	2000US-02295513;
PR	06-SEP-2000;	2000US-0230437;
PR	06-SEP-2000;	2000US-0230438;
PR	08-SEP-2000;	2000US-02311242;
PR	08-SEP-2000;	2000US-02311243;
PR	08-SEP-2000;	2000US-02311244;
PR	08-SEP-2000;	2000US-02311413;
PR	08-SEP-2000;	2000US-02311414;
PR	08-SEP-2000;	2000US-0232080;
PR	08-SEP-2000;	2000US-0232081;
PR	12-SEP-2000;	2000US-02331967;
PR	14-SEP-2000;	2000US-02332397;
PR	14-SEP-2000;	2000US-02332398;
PR	14-SEP-2000;	2000US-02332399;
PR	14-SEP-2000;	2000US-02332400;
PR	14-SEP-2000;	2000US-0232401;
PR	14-SEP-2000;	2000US-0233063;
PR	14-SEP-2000;	2000US-0233064;
PR	14-SEP-2000;	2000US-0233065;
PR	21-SEP-2000;	2000US-02342273;
PR	21-SEP-2000;	2000US-02342274;
PR	25-SEP-2000;	2000US-0234997;
PR	25-SEP-2000;	2000US-0234998;
PR	26-SEP-2000;	2000US-0234584;
PR	27-SEP-2000;	2000US-0235834;
PR	27-SEP-2000;	2000US-0235836;
PR	29-SEP-2000;	2000US-0236327;
PR	29-SEP-2000;	2000US-0236327;
PR	29-SEP-2000;	2000US-0236368;
PR	29-SEP-2000;	2000US-0236369;
PR	29-SEP-2000;	2000US-0236370;
PR	02-OCT-2000;	2000US-0236802;
PR	02-OCT-2000;	2000US-0237037;
PR	02-OCT-2000;	2000US-0237038;
PR	02-OCT-2000;	2000US-0237039;
PR	02-OCT-2000;	2000US-0237040;
PR	13-OCT-2000;	2000US-02399335;
PR	13-OCT-2000;	2000US-0239937;
PR	20-OCT-2000;	2000US-0240960;
PR	20-OCT-2000;	2000US-0241121;
PR	20-OCT-2000;	2000US-0241785;
PR	20-OCT-2000;	2000US-0241786;
PR	20-OCT-2000;	2000US-0241787;
PR	20-OCT-2000;	2000US-0241809;
PR	20-OCT-2000;	2000US-0241826;
PR	01-NOV-2000;	2000US-0244617;
PR	08-NOV-2000;	2000US-0246474;
PR	08-NOV-2000;	2000US-0246475;
PR	08-NOV-2000;	2000US-0246476;
PR	08-NOV-2000;	2000US-0246477;
PR	08-NOV-2000;	2000US-0246478;
PR	08-NOV-2000;	2000US-0246523;
PR	08-NOV-2000;	2000US-0246524;
PR	08-NOV-2000;	2000US-0246525;
PR	08-NOV-2000;	2000US-0246526;
PR	08-NOV-2000;	2000US-0246527;
PR	08-NOV-2000;	2000US-0246528;
PR	08-NOV-2000;	2000US-0246532;
PR	08-NOV-2000;	2000US-0246609;
PR	08-NOV-2000;	2000US-0246610;
PR	08-NOV-2000;	2000US-0246611;
PR	08-NOV-2000;	2000US-0246613;
PR	17-NOV-2000;	2000US-0249207;
PR	17-NOV-2000;	2000US-0249208;
PR	17-NOV-2000;	2000US-0249209;
PR	17-NOV-2000;	2000US-0249210;
PR	17-NOV-2000;	2000US-0249211;
PR	17-NOV-2000;	2000US-0249212;
PR	17-NOV-2000;	2000US-0249214;
PR	17-NOV-2000;	2000US-0249215;
PR	17-NOV-2000;	2000US-0249216;

```
AAC30979
ID AAC30979 standard; cDNA; 361 BP.
AC AAC30979;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 35054.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EF1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST ) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 35054; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 361 BP; 69 A; 100 C; 85 G; 105 T; 2 other;

Query Match 14.0%; Score 33.4; DB 21; Length 361;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 82; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 52 TGGGGTGTGGGCTGGCCCTTGTCTCTTGTGACCCCTCTTGGCAGCTCAGTCAGGACAG 111
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 170 TGGGATCACTTAAGAGATTCTTCTGTGGAACTCAGCTTGGCCTGGACATCAAGAA 229
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 112 GSCCGGTATGACTTTGCAACTGAAGCTGAGGAGTCTTTTCTGACAAATTCCTCTATG 171
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 230 GACCGAGTCTTCTCTGTGCCCCAGGCTGGAGTGGGTGATCTTGGCTCACTGCA 289
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 172 AGTCCAGCTTCTTGGAAATTCCTGAAANATCTGCCTCTCTCTCG 215
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 290 ACCTCCACCTCCCGGTTCAAGTAGATTCCTCTGCTCGCTCAGCCTCC 333
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 13
ABN83971/c
ID ABN83971 standard; DNA; 6855 BP.
XX
AC ABN83971;

XX
DT 06-SEP-2002 (first entry)
XX
DE Human gene sequence #18.
XX
KW Human; brain; tonsil; hippocampus; foetal brain; diagnosis; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 4465..4695
FT /*tag= a
XX
PN WO200252005-A1.
XX
PD 04-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-JP11217.
XX
PR 22-DEC-2000; 2000JP-0389742.
XX
PA (KAZU-) KAZUSA DNA RES INST FOUND.
PA (CELE-) CELESTAR LEXICO-SCI LTD.
XX
PI Ohara O, Nagase T, Nakajima D;
XX
DR WPI; 2002-500762/53.
DR P-PSDB; ABB97951.
XX
PT Genes and their expression products cloned from human cDNA libraries
PT for treatment and diagnosis of diseases associated with their
PT expression -
XX
PS Claim 1(a); Page 136-140; 238pp; Japanese.
XX
CC The invention relates to DNA encoding polypeptides directly cloned from
CC cDNA libraries originating in adult whole brain, human tonsil, human
CC adult hippocampus and human foetal whole brain. Polypeptides and
CC polynucleotides of the invention may be used in the investigation of
CC differential expression of the DNA sequences in normal subjects and
CC disease patients. They may also be used in the production of antibodies,
CC oligonucleotide probes and DNA chips for diagnosis and identification
CC of drugs for treatment of diseases with which the DNA sequences are
CC associated. The sequences given in records ABN83954-ABN83984 represent
CC human gene sequences of the invention.
XX
SQ Sequence 6855 BP; 1752 A; 1535 C; 1489 G; 2079 T; 0 other;

Query Match 13.8%; Score 33; DB 24; Length 6855;
Best Local Similarity 55.3%; Pred. No. 4.1;
Matches 63; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 91 TTGGCAGCTCACATGGAACAGGCGCGGTATGACTTGCACCTGAAGCTGAAGGAGTCTT 150
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 2684 TTCCCACTCCACATCCCCAGGTTTAGTAAGACTTTTCAAAAGCAAGGTAAGGTGAAC 2625
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 151 TTCTGCAAAATTCCTCCATGAGTCCAGCTTCTCTGGAATTCCTGAAANTCTG 204
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 2624 TGTAAGAGAGTTTCATGTATATAAGTACCGCAACTTGTATTCTCTGAAGTCTGTG 2571
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 14
AAV28846
ID AAV28846 standard; DNA; 1128 BP.
XX
AC AAV28846;
XX
DT 03-AUG-1998 (first entry)
XX
DE Mouse coxsackievirus and adenovirus receptor encoding DNA.
XX
KW Mouse; coxsackievirus; adenovirus; receptor; CAR; cardiac infection;
KW myocarditis; pericarditis; dilated cardiomyopathy; meningoencephalitis;
```

KW pancreatic infection; acute pancreatitis; gastrointestinal tract;
XX diabetes mellitus; ss.
OS Mus sp.
XX
XX
FH Key Location/Qualifiers
CDS 1..1128
FT /*tag= a
FT /product= "coxsackievirus and adenovirus receptor"
FT /transl_except= (pos:1096..1098,aa:xaa)
FT /note= "xaa= a stop codon, the sequence is shown as
FT continuing but gets unclear"
XX
XX WO9811221-A2.
PN 19-MAR-1998.
XX
XX
XX 12-SEP-1997; 97WO-US16189.
PF
XX 13-SEP-1996; 96US-0026100.
PR
XX (DAND) DANA FARBER CANCER INST INC.
PA
XX Bergelson JM, Finberg RW, Horowitz MS;
PI
XX WPI; 1998-207384/18.
DR P-FSDB; ANW57213.
XX
XX DNA encoding coxsackie virus and adenovirus receptor - useful for
PT modulation of e.g. cardiac, pancreatic or gastrointestinal infection ,
XX
XX Disclosure; Fig 14; 104pp; English.
XX
XX The present sequence encodes mouse coxsackievirus and adenovirus
CC receptor (CAR). The present invention also describes: (1) a method for
CC modulating CAR expression comprising contacting the cell with an agent
CC which modulates CAR protein activity or CAR nucleic acid expression,
CC such that a cell associated activity is altered relative to a cell
CC associated activity of the cell in the absence of the agent; and (2) a
CC method for detecting the presence of CAR in a biological sample
CC comprising contacting a biological sample with an agent capable of
CC detecting CAR protein or mRNA such that the presence of CAR is detected.
CC Modulation of CAR is useful for treatment of cardiac infection, e.g.
CC myocarditis, pericarditis or dilated cardiomyopathy, or infection of the
CC central nervous system, e.g. a non-specific febrile illness or
CC meningoencephalitis, or pancreatic infection, e.g. acute pancreatitis,
CC or infection of the respiratory or gastrointestinal tract or childhood
CC onset diabetes mellitus. Probes derived from CAR nucleic acids are
CC useful for hybridisation assays, and antibodies raised against CAR
CC protein are useful for blocking CAR expression. Cell-free assays which
CC include combining CAR protein and a candidate/test compound are useful
CC in screening for drugs which interact with CAR protein.
XX
XX Sequence 1128 BP; 297 A; 286 C; 288 G; 257 T; 0 other;
SQ

Query Match 13.4%; Score 32; DB 19; Length 1128;
Best Local Similarity 62.5%; Pred. No. 4.3;
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 33 AGGAGCGCAGTGGCGCTATGGGCTGCGCCCTTGCCCTTGCTGTGACCTCTCT 92
Db 712 ACGATCGCGGGCCCGCTATAGGAGCGCTGCTGGCCCTTGCTGTCATCGGGCCATCTC 771
QY 93 GGCAGCTCACATGGACAGG 112
Db 772 TTCGTGCTCATCAGGAAAGG 791

RESULT 15
ABK09969
ID ABK09969 standard; cDNA; 1251 BP.
XX
XX AC ABK09969;

XX 21-MAY-2002 (first entry)
XX Eastern cottonmouth snake zsnk1 gene sequence.
XX
XX Eastern cottonmouth snake; zsnk1; gene; snake venom; blood pressure;
KW vascular permeability; heparin binding; cell proliferation; mitogenesis;
KW hypotensive; cytostatic; antirheumatic; antiarthritic; antidiabetic;
KW vasotropic; antiarteriosclerotic; vulnery; antiulcer; hepatotropic;
KW antiinflammatory; vaccine; gene therapy; angiogenesis regulator;
KW neurite outgrowth; organ development; organ regeneration; cancer; ss.
XX
XX Aqkistrodon piscivorus piscivorus.
XX
XX Location/Qualifiers
FH Key 201..638
CDS /*tag= a
FT /product= "Eastern cottonmouth snake zsnk1 protein"
FT 201..435
FT misc_feature /*tag= b
FT /note= "Used to make snake venom polypeptide.
FT Specifically claimed in claim 2d"
FT 201..263
FT sig_peptide /*tag= c
FT 201..254
FT sig_peptide /*tag= d
FT /note= "Alternative signal peptide #1"
FT 201..248
FT sig_peptide /*tag= e
FT /note= "Alternative signal peptide #2"
FT 249..435
FT misc_feature /*tag= f
FT /note= "Used to make snake venom polypeptide.
FT Specifically claimed in claim 2c"
FT 249..635
FT mat_peptide /*tag= g
FT /note= "Alternative mature peptide #2"
FT 255..635
FT mat_peptide /*tag= h
FT /note= "Alternative mature peptide #1"
FT 255..435
FT misc_feature /*tag= i
FT /note= "Used to make snake venom polypeptide.
FT Specifically claimed in claim 2b"
FT 264..635
FT mat_peptide /*tag= j
FT 264..435
FT misc_feature /*tag= k
FT /note= "Used to make snake venom polypeptide.
FT Specifically claimed in claim 2a"
XX
XX WO200212334-A2.
XX
XX 14-FEB-2002.
XX
XX 07-AUG-2001; 2001WO-US24999.
XX
XX 07-AUG-2000; 2000US-223164P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO;
XX
XX WPI; 2002-217178/27.
DR P-FSDB; AAU76683.
XX
XX New snake venom zsnk1 polypeptide and polynucleotide, useful for
PT decreasing blood pressure, causing vascular permeability, binding
PT heparin and inducing proliferation or mitogenesis in cells
XX
XX Claim 2; Page 98-99; 103pp; English.
XX
XX The present invention relates to a new snake venom zsnk1 polypeptide
CC

CC comprising amino acid residues 22Val (V)-145V, 19Ser-145V, 17Tyr-145V
CC or 1Met-145V of a sequence comprising 145 amino acids fully defined in
CC the specification. The invention is useful for decreasing blood pressure,
CC causing vascular permeability, binding heparin and inducing proliferation
CC or mitogenesis in cells. Other uses of the invention include regulating
CC organ development and regeneration and in pathological processes where
CC therapeutic treatments or diagnostics are required, including cancer,
CC vasculogenesis and angiogenesis, rheumatoid arthritis, diabetic
CC retinopathy, ischaemic limb disease, vascular disease, myocardial
CC ischaemia, atherosclerosis, haemangioma formation and treating
CC inflammatory disorders including psoriasis. Antibodies of the invention
CC are useful for modulating cardiovascular function and blood pressure,
CC stimulating tissue development or repair, cellular differentiation
CC or proliferation, treatment of full thickness skin wounds including
CC ulcers and skin grafting, to promote vessel repair, and to stimulate
CC haematopoiesis. Antibodies are also useful as anti-venom therapy for
CC snake bite victims, and to diminish pro-fibrotic responses. The present
CC nucleic acid sequence encodes the eastern cottonmouth snake zsnk1
CC protein of the invention.
XX

SQ Sequence 1251 BP; 298 A; 334 C; 325 G; 294 T; 0 other;

Query Match 13.38; Score 31.8; DB 24; Length 1251;
Best Local Similarity 56.18; Pred. No. 5.2;
Matches 60; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 12 CTTTCAGTGTCTCTCCATCCAGGAGCGGCGGCTATGGGCTGTGGGTGGCCGCTT 71

Db 165 CTTCTGAGCAGCTGTGAAGCCAGGAGGAGATAGGCCATGGCTGTACCTGTGGCAGTT 224

QY 72 GTCTCTCTCTGACCTCTTGGCAGCTCACATGGACAGGCGCGG 118

Db 225 GCCATCCCTCTGTGCATCCAGGGCTGGCCATCAGGAGCAGTGC AAG 271

Search completed: May 1, 2003, 03:07:47
Job time : 176.211 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:59:25 ; Search time 781.492 Seconds
(without alignments)
8900.373 Million cell updates/sec

Title: US-09-092-296-1
Perfect score: 239
Sequence: 1 GCCACCGGACTTCAGTGT.....CCCTTCAGGACGACGCTCA 239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_man.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	227	95.0	422	6	AX092334	Sequence
2	227	95.0	422	6	AX376174	Sequence
3	227	95.0	422	6	AX403475	Sequence
4	225.4	94.3	484	6	AX102070	Homo sapi
5	119	49.8	624	6	AX472955	Sequence
6	113.4	47.4	47323	9	AC005937	Homo sapi
7	113.4	47.4	84474	9	AL662854	Human DNA
8	113.4	47.4	104154	2	AL773541	Homo sapi
9	113.4	47.4	156272	9	AL669830	Human DNA
10	113.4	47.4	178688	2	AL713893	Homo sapi
11	113.4	47.4	192650	9	AB023048	Homo sapi
12	113.4	47.4	200000	9	AP000511	Homo sapi
13	68	28.5	349980	6	AX344553	Sequence
14	68	28.5	349980	6	AX344554	Sequence
15	61.2	25.6	349980	6	AX344571	Sequence
16	44.6	18.7	175345	2	AC022301	Mus muscu
17	43.8	18.3	132977	2	RN510D20	Rattus no
18	43.8	18.3	337832	2	AC099175	Rattus no
19	38.2	16.0	130742	2	AP005653	Oryza sat
20	37.8	15.8	185154	2	AC127110	Rattus no
21	36	15.1	155406	2	AC105514	Rattus no
22	35.8	15.0	196840	9	AC104435	Homo sapi
23	35.8	15.0	203773	9	AC097369	Homo sapi
24	35.4	14.8	176994	2	AC118783	Rattus no
25	35.4	14.8	243644	2	AC097608	Rattus no
26	35	14.6	141272	9	AP001976	Homo sapi
27	35	14.6	154937	2	AP002382	Homo sapi
28	35	14.6	202995	2	AC019134	Homo sapi
29	34.8	14.6	188082	2	AC121784	Mus muscu
30	34.8	14.6	188406	2	AC079560	Mus muscu
31	34.8	14.6	197344	2	AC102613	Mus muscu
32	34.8	14.6	203155	2	AC079473	Mus muscu
33	34.8	14.6	292172	2	AC125207	Mus muscu
34	34.6	14.5	77691	9	AC120118	Homo sapi
35	34.6	14.5	100521	9	AC119397	Homo sapi
36	34.6	14.5	173126	9	AC008878	Homo sapi
37	34.4	14.4	2032	9	AK025566	Homo sapi
38	34.4	14.4	77322	9	HS01144C9	Human DNA
39	34.4	14.4	146399	9	AC025835	Homo sapi
40	34.4	14.4	172033	9	AL136131	Human DNA
41	34.4	14.4	177560	2	AC016695	Homo sapi
42	34.4	14.4	189623	2	AC018640	Homo sapi
43	34.4	14.4	193332	2	AL355349	Homo sapi
44	34.4	14.4	219428	9	AC078846	Homo sapi
45	34.4	14.4	333841	2	AL161641	Homo sapi

ALIGNMENTS

RESULT 1
AX092334
LOCUS AX092334 422 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 65 from Patent WO0116318.
ACCESSION AX092334
VERSION AX092334.1 GI:13444481
KEYWORDS human.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 422)
Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0116318-A 65 08-MAR-2001; Genentech, Inc. (US)

FEATURES Location/Qualifiers

source 1..422

BASE COUNT 84 a 134 c 104 g 100 t

ORIGIN

Query Match 95.0%; Score 227; DB 6; Length 422;
Best Local Similarity 99.2%; Pred. No. 4.1e-61;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GGCCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACATATGGGTCTG 60
Db 8 GGCCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACATATGGGTCTG 67

Qy 61 GGCTGCCCTTTGTCCTCTCTTGGACCTTCCTGGCAGCTCACATGGAAACAGGCCGGGTA 120
Db 68 GGCTGCCCTTTGTCCTCTCTTGGACCTTCCTGGCAGCTCACATGGAAACAGGCCGGGTA 127

Qy 121 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
Db 128 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 187

Qy 181 TCCTGGAATTGCTTGA AAAA-NTCTGCTCCTCTTGGACCTTCACATGGAAACAGGCCGGTCA 239
Db 188 TCCTGGAATTGCTTGA AAAAGCTTGCCTCTCTCCATCTCCCTTCAGGAGCAGCGTCA 247

RESULT 2

AX376174

LOCUS AX376174 422 bp DNA linear PAT 01-MAR-2002

DEFINITION Sequence 241 from Patent WO0168848.

ACCESSION AX376174

VERSION AX376174.1 GI:19170479

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and Zhang,Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0168848-A 241 20-SEP-2001; Genentech, Inc. (US)

FEATURES Location/Qualifiers

source 1..422

BASE COUNT 84 a 134 c 104 g 100 t

ORIGIN

Query Match 95.0%; Score 227; DB 6; Length 422;
Best Local Similarity 99.2%; Pred. No. 4.1e-61;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GGCCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACATATGGGTCTG 60
Db 8 GGCCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACATATGGGTCTG 67

Qy 61 GGCTGCCCTTTGTCCTCTCTTGGACCTTCCTGGCAGCTCACATGGAAACAGGCCGGGTA 120
Db 68 GGCTGCCCTTTGTCCTCTCTTGGACCTTCCTGGCAGCTCACATGGAAACAGGCCGGGTA 127

Qy 121 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
Db 128 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 187

Qy 181 TCCTGGAATTGCTTGA AAAA-NTCTGCTCCTCTCCATCTCCCTTCAGGAGCAGCGTCA 239
Db 188 TCCTGGAATTGCTTGA AAAAGCTTGCCTCTCTCCATCTCCCTTCAGGAGCAGCGTCA 247

RESULT 3

AX403475

LOCUS AX403475 422 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 362 from Patent WO0073454.

ACCESSION AX403475

VERSION AX403475.1 GI:21436973

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D., Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P., Grimaldi,C.J., Gurney,A.L., Kijavlin,I., Napier,M.A., Pan,J., Pooni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K., Williams,P., Wood,W.I. and Zhang,Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0073454-A 362 07-DEC-2000; Genentech Inc. (US)

FEATURES Location/Qualifiers

source 1..422

BASE COUNT 84 a 134 c 104 g 100 t

ORIGIN

Query Match 95.0%; Score 227; DB 6; Length 422;
Best Local Similarity 99.2%; Pred. No. 4.1e-61;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GGCCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACATATGGGTCTG 60
Db 8 GGCCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACATATGGGTCTG 67

Qy 61 GGCTGCCCTTTGTCCTCTCTTGGACCTTCCTGGCAGCTCACATGGAAACAGGCCGGGTA 120
Db 68 GGCTGCCCTTTGTCCTCTCTTGGACCTTCCTGGCAGCTCACATGGAAACAGGCCGGGTA 127

Qy 121 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
Db 128 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 187

Qy 181 TCCTGGAATTGCTTGA AAAA-NTCTGCTCCTCTCTCCATCTCCCTTCAGGAGCAGCGTCA 239
Db 188 TCCTGGAATTGCTTGA AAAAGCTTGCCTCTCTCCATCTCCCTTCAGGAGCAGCGTCA 247

RESULT 4

AY102070

LOCUS AY102070 484 bp mRNA linear PRI 18-JUN-2002

DEFINITION Homo sapiens surfactant associated protein G mRNA, partial sequence.

ACCESSION AY102070

VERSION AY102070.1 GI:21464498

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Walker,M.G. and Spiro,P.

TITLE Genes co-expressed with pulmonary surfactants

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 484)

AUTHORS Walker,M.G. and Spiro,P.

TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Incyte Genomics, 1475 Flamingo Way,
Sunnyvale, CA 94087-3405, USA
FEATURES
source Location/Qualifiers
1..484
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="236582"
c1..>484
/gene="surfactant associated protein G"
/note="SFTPRG"
BASE COUNT 124 a 149 c 110 g 101 t
ORIGIN
Query Match 94.3% Score 225.4; DB 9; Length 484;
Best Local Similarity 98.8%; Pred. No. 1.3e-60;
Matches 237; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 GCCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGTCTG 60
|||||
Db 5 GCCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGTCTG 64
QY 61 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGGCAGCTCACATGGAACAGGCGCGGTA 120
|||||
Db 65 GGCTGCCCTTGTCTCTCTGACCTCTCTGGCAGCTCACATGGAACAGGCGCGGTA 124
QY 121 TGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
|||||
Db 125 TGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 184
QY 181 TCCTGGAATGTGTTGAAA-NCTCGCTCCTCTCCATCTCCCTTCAGGACACAGCTCA 239
|||||
Db 185 TCCTGGAATGTGTTGAAAAGTCTGCTCTCTCTCCATCTCCCTTCAGGACACAGCTCA 244
RESULT 5
AX472955 AX472955 624 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 4 from Patent WO0218576.
ACCESSION AX472955
VERSION AX472955.1 GI:22207742
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Chen,S.Y., Macina,R.A., Sun,Y. and Recipon,H.
Compositions and methods relating to lung specific genes
Patent: WO 0218576-A 4 07-MAR-2002;
Diadexus, Inc. (US)
FEATURES
source Location/Qualifiers
1..624
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 129 a 175 c 182 g 138 t
ORIGIN
Query Match 49.8% Score 119; DB 6; Length 624;
Best Local Similarity 98.5%; Pred. No. 8.9e-27;
Matches 130; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 109 CAGGCGGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCCT 168
|||||
Db 314 CAGGCGGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCCT 373
QY 169 ATGAGTCCAGCTTCTCGAATGCTGAAAA-NCTCGCTCCTCTCCATCTCCCTTCAG 227
|||||
Db 374 ATGAGTCCAGCTTCTCGAATGCTGAAAAAGCTCTGCTCTCTCTCTCTCTCTCTCTCAG 433
QY 228 GGACACGCTCA 239
|||||
Db 434 GGACACGCTCA 445

RESULT 6
AC005937 AC005937 47323 bp DNA linear PRI 05-NOV-1998
LOCUS Homo sapiens clone UWGC:370M23.002 from 6p21, complete sequence.
DEFINITION AC005937
ACCESSION AC005937.1 GI:3845393
VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 47323)
Geraghty,D.E.
Large scale sequence analysis of the human MHC class I region
Unpublished (1998)
JOURNAL Fred Hutchinson Cancer Research Center
REMARK The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
2 (bases 1 to 47323)
Geraghty,D.E. and Olson,M.V.
Direct Submission
Submitted (05-NOV-1998) Human Genome Center, University of
Washington, Box 352145, Seattle, WA 98195, USA
JOURNAL University of Washington Human Genome Center
REMARK Box 352145 Seattle, WA 98195
Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
Overlapping Sequences:
5': UWGC:370M23.013 (Genbank Accession: AC005530)
3': UWGC:y67c112 (Genbank Accession: AC004211)
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
Double stranded (DS) coverage: 75.5%
DS or two chemistry coverage: 98.9%
Single stranded regions: 3
Sequence Validation:
This sequence has been validated by Multiple Complete Digest
Mapping. Comparison of the experimentally derived map digest
fragments with sequence-predicted fragments is given below.
Small fragments below a variable cutoff (approximately 400-600bp)
are not mapped and hence do not appear in the table. There are no
significant remaining discrepancies between the experimental and
predicted values. Uniquely ordered fragment groups are separated
by dashed lines.
BglII HindIII NsiI
Map Seq Map Seq Map Seq
1069.11 1050.00 889.55 866.00 30541.40 30653.00
20320.67 20855.00 1050.18 1015.00 3279.08 3231.00
2171.50 2147.00 7268.78 7196.00
2560.20 2531.00 10085.80 9952.00
4335.42 4269.00 11212.78 11131.00
2698.62 2628.00
1927.50 1887.00

BASE COUNT 19363 a 22004 c 21777 g 21330 t
ORIGIN

Query Match 47.4%; Score 113.4; DB 9; Length 84474;
Best Local Similarity 95.1%; Pred. No. 8e-25;
Matches 117; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGTCG 60
|||||
Db 56564 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGTCG 60
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QY 61 GGTGCCCCCTTGTCTCTTGGACCCCTCTTGGACCTCACATGGAACAGGCCGGGTA 120
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Db 56504 GGTGCCCCCTTGTCTCTTGGACCCCTCTTGGACCTCACATGGAACAGGTGAGGCT 56445
|||||

QY 121 TGA 123
||
Db 56444 AGA 56442

RESULT 8
AL773541
LOCUS
DEFINITION Homo sapiens chromosome 6 clone XXbac-11J22, linear HTG 09-AUG-2002
AL773541 104154 bp DNA linear HTG 09-AUG-2002
PROGRESS ***, in ordered pieces.
ACCESSION AL773541
VERSION AL773541.4 GI:22204637
KEYWORDS HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Almeida, J.
Direct Submission
Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk
On Aug 11, 2002 this sequence version replaced gi:21621737.
***** Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquerry@sanger.ac.uk
***** Project Information
Center project name: bQb1J22
***** Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 104135 bases at least Q40
Consensus quality: 104142 bases at least Q30
Consensus quality: 104145 bases at least Q20
Insert size: 104154; sum-of-contigs
Insert size: 110727; 1.1% error; agarose-fp
Quality coverage: 19.52x in Q20 bases; sum-of-contigs Quality
coverage: 18.64x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-11J22"
/clone.lib="DNA-arts-BAC.1-QBL.1"
misc_feature 1..104154
/note="assembly_fragment:00090"

BASE COUNT 26560 a 25418 c 26095 g 26083 t
ORIGIN

Query Match 47.4%; Score 113.4; DB 2; Length 104154;
Best Local Similarity 95.1%; Pred. No. 8.2e-25;
Matches 117; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGTCG 60
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Db 67498 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGTCG 67557
|||||

QY 61 GGTGCCCCCTTGTCTCTTGGACCCCTCTTGGACCTCACATGGAACAGGCCGGGTA 120
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Db 67558 GGTGCCCCCTTGTCTCTTGGACCCCTCTTGGACCTCACATGGAACAGGTGAGGCT 67617
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QY 121 TGA 123
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Db 67618 AGA 67620

RESULT 9
AL669830/c
LOCUS
DEFINITION Human DNA sequence from clone XXbac-118E17 on chromosome 6,
complete sequence.
AL669830
VERSION AL669830.9 GI:20135762
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Johnson, C.
Direct Submission
Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk
On Apr 10, 2002 this sequence version replaced gi:20067510.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
from a CHORI-501 human bac - PGF cell line library VECTOR:
PTARBAC2.1

This sequence was generated from part of bacterial clone contigs
constructed by the MHC Haplotype Consortium and collaborators.
Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr6/MHC>.

FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-118E17"
/clone.lib="CHORI-501"
BASE COUNT 41135 a 37989 c 36907 g 40241 t
ORIGIN

Query Match 47.4%; Score 113.4; DB 9; Length 156272;
Best Local Similarity 95.1%; Pred. No. 8.5e-25;
Matches 117; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

misc_feature	1..37410	/note="assembly_fragment:03218 fragment_chain:1"
misc_feature	37511..82372	/note="assembly_fragment:00918 fragment_chain:1"
misc_feature	82473..142457	/note="assembly_fragment:03231 fragment_chain:1"
misc_feature	142558..152859	/note="assembly_fragment:03008 fragment_chain:1"
misc_feature	152960..172054	/note="assembly_fragment:04309 fragment_chain:1"
misc_feature	172155..178688	/note="assembly_fragment:03507 fragment_chain:1 clone_end:17 vector_side:right"
BASE COUNT	46316 a 40707 c 42166 g 48998 t	501 others
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Best Local Similarity	95.1%	Pred. No. 8.6e-25;
Matches 117;	Conservative 0;	Mismatches 6; Indels 0; Gaps 0;
QY	1	GGCCACCGGACCTTCAGTGTCTCTCCATCCACGAGGCGCAGTGGCCACTATGGGTCG 60 Db 173447
QY	61	GGCTGCCCTTGTCTCCTCTTGTACCCCTCTTGGCAGCTCACATGACGAGCCGGGTA 120 Db 173507
QY	121	GGCTGCCCTTGTCTCCTCTTGTACCCCTCTTGGCAGCTCACATGACGAGCGGCT 173566 Db 173567
AGT	121	GGCTGCCCTTGTCTCCTCTTGTACCCCTCTTGGCAGCTCACATGACGAGCGGCT 173566 Db 173567
RESULT 11		
AB023048		
LOCUS	AB023048	192650 bp DNA linear PRI 20-NOV-1999
DEFINITION	AB023048	Human sapiens genomic DNA, chromosome 6p21.3, HLA class I region, clone:5319, complete sequence.
ACCESSION	AB023048.1	GI:5672603
VERSION	AB023048	HTG.
KEYWORDS	AB023048	HTG.
SOURCE	AB023048	Human sapiens cell_line:978SK DNA, clone:5319.
ORGANISM	AB023048	Human sapiens
REFERENCE	AB023048	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	AB023048	Shiina, T., Taniya, G., Oka, A., Takishina, N., Yamagata, T., Kikkawa, E., Iwata, K., Tomizawa, M., Okuaki, N., Kuwano, Y., Watanabe, K., Fukuzumi, Y., Iwakura, S., Sugawara, C., Ono, A., Yamazaki, M., Tashiro, H., Ando, A., Ikemura, T., Soeda, E., Kimura, M., Babram, S. and Inoko, H.
TITLE	AB023048	Molecular dynamics of MHC genesis unraveled by sequence analysis of the 1,796,938-bp HLA class I region
JOURNAL	AB023048	Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
MEDLINE	AB023048	20027539
REFERENCE	AB023048	2 (bases 1 to 192650)
AUTHORS	AB023048	Shiina, T. and Takishina, N.
TITLE	AB023048	Direct Submission
JOURNAL	AB023048	Submitted (29-JAN-1999) Takashi Shiina, Tokai University School of Medicine, Department of Molecular Life Science 2; Bohseidai, Isehara, Kanagawa 259-1193, Japan (E-mail:tshina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,

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    Fax:81-463-94-8884)
    Location/Qualifiers
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        /chromosome="6"
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        /clone="53L9"
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BASE COUNT 49862 a 44743 c 45833 g 52212 t
ORIGIN
Query Match 47.4%; Score 113.4; DB 9; Length 192650;
Best Local Similarity 95.1%; Pred. No. 8.6e-25;
Matches 117; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GGCCACGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTG 60
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Db 177631 GGCCACGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTG 177690
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QY 61 GGCTGCCCTTGTCTCTTGTGACCTCTCTTGGCAGCTCACATGGAACAGGCGCGGTA 120
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QY 121 TGA 123
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Db 177751 AGA 177753

RESULT 12
APO00511
LOCUS APO00511 200000 bp DNA linear PRI 22-AUG-2001
DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
section 10/20
ACCESSION AP000511 BA000025
VERSION AP000511.1 GI:5926698
KEYWORDS
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Shilina,S., Tamiya,G., Oka,A. and Inoko,H.
Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region
Published Only in Database (1999)
JOURNAL
2 (bases 1 to 200000)
Submitted (21-SEP-1999)
AUTHORS HiraKawa,M., Yamaguchi,H., Imai,K. and Shimada,J.
Direct Submission
TITLE
JOURNAL
CORPORATION (JST), Advanced Databases Department; 5-3, Yonbancho,
Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@tokyo.jst.go.jp,
URL:http://www.alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
Fax:81-3-5214-8470)
This sequence is conducted by Tokai University as a JST sequencing
Team.
COMMENT
Principal Investigator: Hidetoshi Inoko Ph.D
Phone:+81-463-93-1121, Fax:+81-463-94-8884,
The sequence is submitted by Human Genome Sequencing in ALIS
project of JST
Japan Science and Technology Corporation (JST)
5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan
For further information about this sequences, please visit our
sequence archive Web site (http://www.alis.tokyo.jst.go.jp/HGS/top.
html) or send email to webmaster@www.alis.tokyo.jst.go.jp.
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    /note="SHGC-12985;The location is between each flanking
FEATURES
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    of PCR primers."
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    /note="Cda0vh10;The location is between each flanking site
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    /db_xref="GB:443382"
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    129637..129767,129949..130081,130328..130411,
    130596..130664,130826..130937,131154..131242,
    131334..131430,132032..132163,132556..132660,
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    131154..131242,131334..131430,132032..132163,
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    /gene="TFIIH"
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    /product="Transcription factor II H"
    /protein_id="BA86317.1"
    /db_xref="GI:15277224"
    /translation="MESTPSRGLNRVHLQCRNLQELGLSPGVLDRLYGHPTATCLAV
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    GGLQGLINPFRQNLRIALLGGKAWSDDTSQLGPKHARDVPSLDKVAERWEVLQ
    HFMYGSPSAVSDLAQLLSQGLKMSDTEFPPEPCITSAQFQFLDTPAQLWYFMQLQ
    YLQTAQSGMDLVEILSELSFQSLSTLKGDSVEGMSDLSLNFQLHRLRFFGLVQFQRK
    KSRYYPTLAINLSGVSAGVTGHPQGFIVVETNRYLAYTSEQLALALFSEM
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148927..149022,149548..149794,149902..150089,
150614..150712,150972..151119,152662..152890,
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/gene="DDR"
141936..142934
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/note="SHGC-16870;the location is between each flanking
site of PCR primers."
/db_xref="GDB:741215"
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/note="RH18132;The location is between each flanking site
of PCR primers."
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145225..145469,146576..146686,147419..147584,
148667..148818,148927..149022,149548..149794,
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152662..152890,153082..153184,153278..153362))
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143783..144017,14493..144711,144949..145076,
145225..145469,146576..146686,147419..147584,
148667..148818,148927..149022,149548..149794,
149902..150089,150614..150712,150972..151119,
152662..152890,153082..153184,153278..153362))
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/product="Receptor tyrosine kinase"
/protein_id="BAB63318.1"
/db_xref="GI:15277225"
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QQRHAGGKFEFSYRLRYSRDGRWGWKDRWGOEIVSGNDEPGCVLKDLPMPV
ARLVFPRADRVMSVCLVELYGLMRDGLSYTADPGQWYLSYAVYLNDSYDGH
TVGLOVGGIQLQADGVGLDDFKRSQELRWGIDYVGNHSSFGSYVEFEFDR
LAFQAMQVCHNNHILGARLPFGVECFRRFGPAMWEGEPMRHNLGNLGDPRARV
PLPGLRVARPLQCRFLFAGPMLLFSEISFISDVNNSSPALGTFPPAPMPPPGPP
TFPSLELEPRGQPVAKAESGTAILIGCLVAIILLILLIALLMWRHLRLLSKA
ERVLEELAVHLSVPDITILNNRPGPREPPYQEPFRPNPPHSPVCPNGSALLL
PHYAVLLATVYARRPGPGPTPAWAKPTNTQASGDYMEPKPGAPLPPPPQNSV
PHYAEADITVLTQGTGTNTYAVPALPVCAGVDGPRVDPPRSLRFEKELGEGQGEV
HUCVRLGVCQDDPLDLPLNVRKHGHLVAVKILRPDANKARNDFLKVYIKMSRLKP
NIIRLLGVQDDPLDITDYMENDLNQFLSAHLEDKAEAGAPGQAAGPTISY
PMLHVAQIASGRYLAIFNFIHRDLATNCLVGENFTIKIADFGRMSAGQIYR
VGRVAVLPFRMAWECILMGKFTTASDWAFVGTLMWELMCLRCAPGQQTDEQVFN
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Best Local Similarity 95.1%; Pred. No. 8.6e-25;
Matches 117; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACACGGGACTTCAGTGTCTCTCCATCCACGAGGAGCGAGTGGCCACATATGGGGTCTG 60
Db 109958 GGCCACCGGACTTCAGTGTCTCTCCATCCACGAGGAGCGAGTGGCCACATATGGGGTCTG 110017

QY 61 GCCTGCCCCCTTGTCTCTCTGTGACCTCTCTGGCAGCTCACATGGAACAGGCGCGGTGTA 120
Db 110018 GCGTGCCCCCTTGTCTCTCTGTGACCTCTCTGGCAGCTCACATGGAACAGGCGGTGTA 110077

QY 121 TGA 123
Db 110078 AGA 110080

RESULT 13
AX344553/c
LOCUS      AX344553      349980 bp      DNA      linear      PAT 01-FEB-2002
DEFINITION Sequence 4 from Patent WO0200932.
ACCESSION  AX344553
VERSION     AX344553.1  GI:18492439
KEYWORDS    .
SOURCE      Synthetic construct.
ORGANISM    Synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Olek.A., Piepenbrock,C. and Berlin,K.
TITLES      Diagnosis of known genetic parameters within the mhc
JOURNAL     Patent: WO 0200932-A 4 03-JAN-2002;
            Epigenomics AG (DE)
FEATURES    Location/Qualifiers
             source
               1..349980
               /organism="synthetic construct"
               /db_xref="taxon:32630"
               /note="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-Original length of seq 2: 3.673778 <223>-split as follows.-seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 2.749.980-seq 23 2.700.001 3.049.980-seq 24 3.000.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.673.778"

BASE COUNT      86882 a 5859 c 85073 g 172166 t
ORIGIN

Query Match      28.5%; Score 68; DB 6; Length 349980;
Best Local Similarity 76.9%; Pred. No. 2.4e-10;
Matches 83; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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Db 319859 CCACCGAAGCTTCATATCTCTCTCCCAAAAGCGCAATTAACCACTATAAATCTAAA 319800
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QY 63 CTGCCCCCTGTGCTCTCTTGACCCCTCTGGCAGCTCACATGGAACA 110
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Db 319799 CTACCCCTTATCCTCTCTTAACCTCTTAACAACCTCACATAAAACA 319752
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RESULT 14
AX344554/c 349980 bp DNA linear PAT 01-FEB-2002
LOCUS AX344554
DEFINITION Sequence 5 from Patent WO0200932.
ACCESSION AX344554
VERSION AX344554.1 GI:18492440
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.
REFERENCE
1
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 5 03-JAN-2002;
Epigenomics AG (DE)
FEATURES
Location/Qualifiers
1..349980
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-original length of seq 2: 3.673778 <223>-split as follows.-seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 2.749.980-seq 23 2.700.001 3.049.980-seq 24 3.000.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.673.778"
BASE COUNT 92349 a 5068 c 82248 g 170315 t
ORIGIN

Query Match 28.5%; Score 68; DB 6; Length 349980;
Best Local Similarity 76.9%; Pred. No. 2.4e-10;
Matches 83; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 3 CCACGGGACTTCAGTCTCTCCTCCATCCAGGAGCGAGTGGCCACTATGGGCTGGG 62
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Db 19859 CCACCGAAGCTTCATATCTCTCTCCCAAAAGCGCAATTAACCACTATAAATCTAAA 19800
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QY 63 CTGCCCCCTGTGCTCTCTTGACCCCTCTGGCAGCTCACATGGAACA 110
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Db 19799 CTACCCCTTATCCTCTCTTAACCTCTTAACAACCTCACATAAAACA 19752
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RESULT 15
AX344571 349980 bp DNA linear PAT 01-FEB-2002
LOCUS AX344571
DEFINITION Sequence 22 from Patent WO0200932.
ACCESSION AX344571
VERSION AX344571.1 GI:18492457
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.
REFERENCE
1
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
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TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 22 03-JAN-2002;
Epigenomics AG (DE)
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